

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2004, 21:27:04 ; Search time 23 Seconds
(without alignments)
965.181 Million cell updates/sec

Title: US-09-700-696C-2
Perfect score: 2279
Sequence: 1 VNKKEYSISNKTENHGLRMS.....RQDSESSGSSGSSSDGD 430

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/1aa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/5C COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/5D COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/5E COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/5F COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2276	99.9	525 4	US-10-132-920B-27 Sequence 27, Appl
2	2157	94.6	430 4	US-10-132-920B-2 Sequence 2, Appl
3	140	6.1	772 1	US-08-524-757-12 Sequence 12, Appl
4	136	6.0	1187 1	US-08-320-559-28 Sequence 28, Appl
5	136	6.0	1187 3	US-08-545-860D-28 Sequence 28, Appl
6	136	6.0	1187 3	PCT-US94-0496-28 Sequence 28, Appl
7	136	6.0	1210 1	US-08-320-559-26 Sequence 26, Appl
8	136	6.0	1210 3	US-08-545-860D-26 Sequence 26, Appl
9	136	6.0	1210 5	PCT-US94-0496-26 Sequence 26, Appl
10	135.5	5.9	723 1	US-07-814-964-11 Sequence 11, Appl
11	135.5	5.9	723 1	US-08-258-442-11 Sequence 11, Appl
12	135.5	5.9	723 1	US-08-328-809-6 Sequence 6, Appl
13	135.5	5.9	723 4	US-08-866-840-6 Sequence 6, Appl
14	135.5	5.9	723 4	PCT-US92-1107-11 Sequence 11, Appl
15	135.5	5.9	723 5	US-09-386-962C-4 Sequence 4, Appl
16	135.5	5.9	1742 4	US-09-386-962C-4 Sequence 4, Appl
17	134.5	5.9	1115 2	US-08-487-826B-2 Sequence 2, Appl
18	134.5	5.9	1115 2	US-08-487-826B-2 Sequence 2, Appl
19	134.5	5.9	1115 4	US-09-210-288-2 Sequence 2, Appl
20	128	5.6	703 3	US-08-910-925-4 Patent No. 5198347
21	127.5	5.6	1235 1	US-08-118-101A-2 Sequence 4, Appl
22	126.5	5.6	455 5	PCT-US93-07261-13 Sequence 13, Appl
23	126.5	5.6	1663 3	PCT-US93-07261-16 Sequence 16, Appl
24	125.5	5.5	1261 3	US-09-208-742-4 Sequence 4, Appl
25	125.5	5.5	1261 4	US-09-332-295-2 Sequence 2, Appl
26	125.5	5.5	1261 4	US-09-709-979-2 Sequence 2, Appl
27	125.5	5.5	1261 4	US-10-147-268-2 Sequence 2, Appl

28	124.5	5.5	1183 4	US-09-134-001C-3530 Sequence 3530, Ap
29	123	5.4	493 3	US-08-999-774A-12 Sequence 12, Appl
30	123	5.4	1177 5	US-09-134-001C-5106 Sequence 5106, Ap
31	123	5.4	1588 4	PCT-US93-07261-11 Sequence 11, Appl
32	122	5.4	690 4	US-09-134-001C-4568 Sequence 4568, Ap
33	121.5	5.3	754 4	US-09-976-594-375 Sequence 375, Ap
34	121	5.3	1404 4	US-08-801-308-1 Sequence 1, Appl
35	120.5	5.3	1435 2	US-08-568-459A-4 Sequence 4, Appl
36	120.5	5.3	1435 2	US-08-487-826B-4 Sequence 4, Appl
37	120.5	5.3	1250 4	US-09-210-288-4 Sequence 4, Appl
38	120	5.3	1250 1	US-08-441-139-9 Sequence 9, Appl
39	120	5.3	2842 1	US-07-741-940-7 Sequence 7, Appl
40	120	5.3	2842 1	US-08-289-548A-7 Sequence 7, Appl
41	120	5.3	2842 1	US-08-452-654-7 Sequence 7, Appl
42	120	5.3	2842 4	US-08-449-731-7 Sequence 7, Appl
43	120	5.3	2843 1	US-07-741-940-2 Sequence 2, Appl
44	120	5.3	2843 1	US-08-289-548A-2 Sequence 2, Appl
45	120	5.3	2843 1	US-08-452-654-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-10-132-920B-27
; Sequence 27, Application US/10132920B
; Patent No. 6673900
; GENERAL INFORMATION:
; APPLICANT: Rowe, Peter
; TITLE OF INVENTION: A Polypeptide Hormone-Phosphatoin
; FILE REFERENCE: BEAR-0050CN
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 09/434,185
; PRIOR FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-132-920B-27

Query Match 99.9%; Score 2276; DB 4; Length 525;
Best Local Similarity 99.8%; Pred. No. 1.3e+186;
Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	VNKKEYSISNKTENHGLRMSIYKSTGKNGFEDGDDAISKLHDOREYGAALIRNNCHIM	60
DB	96	VNKKEYSISNKTENHGLRMSIYKSTGKNGFEDGDDAISKLHDOREYGAALIRNNCHIM	155
QY	61	GPVTAIKLIGENKENTPNTVNIIPASMTYAKASDKKKPQRDSQAOKSPVSKSTHR	120
DB	156	GPVTAIKLIGENKENTPNTVNIIPASMTYAKASDKKKPQRDSQAOKSPVSKSTHR	215
QY	121	IQHNIDYVHLKSKVKKIPSDFFGSGYTDIQEFGNDISPFSGDQPFQDIPEKGATGPD	180
DB	216	IQHNIDYVHLKSKVKKIPSDFFGSGYTDIQEFGNDISPFSGDQPFQDIPEKGATGPD	275
QY	181	LEKDIQTGFAGSEASETHLDTKKRGVYIEPERENGANTIGTDETAKEADAVSVLY	240
DB	276	LEKDIQTGFAGSEASETHLDTKKRGVYIEPERENGANTIGTDETAKEADAVSVLY	335
QY	241	EGSNDIMGSIKELPGRGNRVDAQSQAHAQKVEFYPPAPSKKREKSGSDAASFN	300
DB	336	EGSNDIMGSIKELPGRGNRVDAQSQAHAQKVEFYPPAPSKKREKSGSDAASFN	395
QY	301	YNELPKKGKSTKGVDSNRNOATLNEKORPFSKKSQGLPSPHGLNELLKNEVDSFN	360
DB	396	YNELPKKGKSTKGVDSNRNOATLNEKORPFSKKSQGLPSPHGLNELLKNEVDSFN	455
QY	361	GPSHENITTHGRKYVYVPHRNNSTNKKMPQCKGSGWGPSPHNRFPSSRRRDSSESD	420

Db 456 GPHENITTHGRKHYVPHRÖNNSTNNKGMPOGKSGWGRPHSNRRFSSRRDDSESSD 515
 QY 421 SSSSSSSDGD 430
 Db 516 SSSSSSSDGD 525

RESULT 2
 US-10-132-920B-2
 ; Sequence 2, Application US/10132920B
 ; Patent No. 6673900
 ; GENERAL INFORMATION:
 ; APPLICANT: Rowe, Peter
 ; TITLE OF INVENTION: A Polypeptide Hormone-Phosphatonic
 ; FILE REFERENCE: BEAR-005CON
 ; CURRENT FILING DATE: 2002-04-25
 ; PRIOR APPLICATION NUMBER: 09/434,185
 ; NUMBER OF SEQ ID NOS: 55
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 430
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-10-132-920B-2

Query Match 94.6%; Score 2157; DB 4; Length 430;
 Best Local Similarity 92.8%; Pred. No. 1.5e-176;
 Matches 414; Conservative 0; Mismatches 0; Indels 32; Gaps 2;

QY 1 VNKEYSISNKNENTNGLKMSIYPTKSTGKGFEDGDDAISKLHDEEYGAALIRNMQHIM 60
 Db 1 VNKEYSISNKNENTNGLKMSIYPTKSTGKGFEDGDDAISKLHDEEYGAALIRNMQHIM 60
 QY 61 GPVTAIKLGEENKENTPRVLTNIIPASMTAKAKSKDKKPPORDSOAKSPVYSKSTHR 120
 Db 61 GPVTAIKLGEENKENTPRVLTNIIPASMTAKAKSKDKKPPORDSOAKSPVYSKSTHR 120
 QY 121 IQHNIDYKHLKSKVKKIPSDPEGSGYTDLOERGNDNISPF-----SGDG 164
 Db 121 IQHNIDYKHLKSKVKKIPSDPEGSGYTDLOERGNDNISPF-----SGDG 164
 QY 121 IQHNIDYKHLKSKVKKIPSDPEGSGYTDLOERGNDNISPF-----SGDG 180
 Db 121 IQHNIDYKHLKSKVKKIPSDPEGSGYTDLOERGNDNISPF-----SGDG 180
 QY 165 QPFKIDPKGKGTGPDLEGKDIQTGFAPSEASTHLDTKPKGYNEIPEREENGANTIGT 224
 Db 165 QPFKIDPKGKGTGPDLEGKDIQTGFAPSEASTHLDTKPKGYNEIPEREENGANTIGT 224
 QY 181 QPFKIDPKGKGTGPDLEGKDIQTGFAPSEASTHLDTKPKGYNEIPEREENGANTIGT 224
 Db 181 QPFKIDPKGKGTGPDLEGKDIQTGFAPSEASTHLDTKPKGYNEIPEREENGANTIGT 224
 QY 225 RDETAKEADAVDVSLVEGSDIMGSTNFKELPGREGNFRVDAGSQNAHQGVETFPYPPAPS 284
 Db 225 RDETAKEADAVDVSLVEGSDIMGSTNFKELPGREGNFRVDAGSQNAHQGVETFPYPPAPS 284
 QY 285 KEKKEGSSDAESTNNYNEIPKNGKSTRKGVDSNRNQAATLNEKORPFSKSGQGLPIP 344
 Db 285 KEKKEGSSDAESTNNYNEIPKNGKSTRKGVDSNRNQAATLNEKORPFSKSGQGLPIP 344
 QY 345 SRGLDNEIKNEMDSFNGPSHENITTHGRKHYVPHRÖNNSTNNKGMPOGKSGWGRPHSN 404
 Db 345 SRGLDNEIKNEMDSFNGPSHENITTHGRKHYVPHRÖNNSTNNKGMPOGKSGWGRPHSN 404
 QY 405 RRFSSRRDDSESSDSSSSSSDGD 430
 Db 405 RRFSSRRDDSESSDSSSSSSDGD 430

RESULT 3
 US-08-524-757-12
 ; Sequence 12, Application US/08524757
 ; Patent No. 5792634
 ; GENERAL INFORMATION:
 ; APPLICANT: Conaway, Ronald C.
 ; APPLICANT: Conaway, Joan W.
 ; APPLICANT: Bradsher, John N.
 ; TITLE OF INVENTION: RNA Polymerase Transcription Factor

NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: RICHARDS, MEDLOCK & ANDREWS
 STREET: 1201 Elm Street, Suite 4500
 CITY: Dallas
 STATE: TX
 COUNTRY: US
 ZIP: 75270-2197
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/524,757
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/13621
 FILING DATE: 29-NOV-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/160087
 FILING DATE: 30-NOV-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Haire, John A.
 REGISTRATION NUMBER: 37,345
 REFERENCE/DOCKET NUMBER: B35006CIPCIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (214) 939-4500
 TELEFAX: (214) 939-4600
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 772 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ; US-08-524-757-12

Query Match 6.1%; Score 140; DB 1; Length 772;
 Best Local Similarity 20.5%; Pred. No. 0.0017;
 Matches 87; Conservative 49; Mismatches 144; Indels 144; Gaps 17;

QY 23 PSTGKGFEDGDDAISKLHDEEYGAALIRNMQHIMGPVTAIKLGEENKENTPRVLT 82
 Db 210 PGKGSNAFOQLRGLASOERHLEPFGKGVYQNKER----- 245
 QY 83 NIIPASMTAKAKSKDKKPPORDSOAKSPVYSKSTHRIQHNIDYKHLKSKVKKIPSDPE 142
 Db 246 -----KSHDKRVDKAKDEKASVYSREKSH-----KALSK----- 277
 QY 143 GSGYTDLOERGNDISPFSGDQPPKDIIPKGEATGPDLEGKDIQTGFAPSEASTHL 201
 Db 278 -----EENRPPSGDNAREKP--FSSGVKKEKREGSLKKCLPSEASDNL 325
 QY 202 DTGKPGYNEIPEREENGANTIGRDETAKEADAVDVSLVEGSDIM-----GSTNFKEL 255
 Db 326 --KKPGRD--PEAK-----LDKSKGGLDSFTDG--KAGDILLPKYKSGSNLKT 372
 QY 256 PREGNFRVDAGSQNAHQGV-----EFHYD-----PAPSKKEGSSDAES 298
 Db 373 EGVKTNLDRKSLGS--LPKVEETDMEDEFEQPTMSFESYLSYDQPKKKKIVKT-SATA 430
 QY 299 TYNNEIPKNGKSTRKGVDSNRNQAATLNEKORPFSKSGQGL----- 341
 Db 431 LGDKGLKRDKSGTGNLDSVQGLPKVNTKSEKPGADLAKLRKVPDVLPTLPDLPLPA 490
 QY 342 -----PIPSRGDNEIKNEMDSFNGPSHEN-----ITTHGRKHYVPHRÖNN 378
 Db 491 IQANVPLPLBELISSFQPKRAFSPOEEBAGFTGRMMRMQVYSGSKCAYLPKXMT 550
 QY 379 -HRQ 381
 Db 551 LHOQ 554

RESULT 4

US-08-320-559-28
Sequence 28, Application US/08320559
Patent No. 5633135

GENERAL INFORMATION:

APPLICANT: Croce, Carlo
APPLICANT: Cnaan, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
TITLE OF INVENTION: Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
TITLE OF INVENTION: All-1 Region
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 5633135
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,559
FILING DATE:
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/062,443
FILING DATE: 14 MAY 1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/971,094
FILING DATE: 30-OCT-92

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,830
FILING DATE: 27-MAY-92

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/805,093
FILING DATE: 11-DEC-91

ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0855

TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO. 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 1187 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-320-559-28

Query Match 6.0%; Score 136; DB 1; Length 1187;
Best Local Similarity 20.6%; Pred. No. 0.007;
Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;

QY 92 AKAHKDKKKKPPORDS-----QACKSPVSKSTRICHINIDYLKHLSTVK 135
DB 530 SEHSESKDPPKSSSKAPRAPEAPHGKSCQSPAQGPBPQQTGTGTPK-----K 584
QY 136 KIPSPFEGSGYTDLCERGNDNISPSGQGPFXDIP-----GKGE-----ATGPD 181
DB 585 PVKASAPAGSRTSLQGEREPGLPYGSRDQTSKDPKVKTKGRPRMAASNEPKPAVPSS 644
QY 183 ECKDQGTGAPGSEAS-----THDTPKKPGY-----NEIPEREENGNTTGTDE 227
DB 645 EKKKHKSLPAPSKALSGPEPAKDNVEDTPEHFLVPLTESQGPFGSGSGRTSGCQA 704

RESULT 5

US-08-545-860D-28
Sequence 28, Application US/08545860D
Patent No. 6040140

GENERAL INFORMATION:

APPLICANT: Croce, Carlo
APPLICANT: Cnaan, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESS: Woodcock Washburn, Kurtz, Mackiewicz &
ADDRESS: No. 6040140
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,860D
FILING DATE: 07-MAR-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
FILING DATE: 22-APR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/10930
FILING DATE: 09-DEC-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/327,392
FILING DATE: 19-OCT-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/320,559
FILING DATE: 11-OCT-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/062,443
FILING DATE: 14-MAY-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/971,094
FILING DATE: 30-OCT-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,839
FILING DATE: 27-MAY-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/805,093
FILING DATE: 11-DEC-1991

ATTORNEY/AGENT INFORMATION:
NAME: Deluca Esq., Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1262

QY 228 TAKEADAVDVLVSGSNDIMGSTNFKELPGRBNV-----DAGSQAHQKVE 276
DB 705 VVQEDSRKDRPLPLPDLTKLSPLRDPPEPQSLMKITDLSRLTPPGKSGRRQKAE 764
QY 277 FHYPPAPSKERKKGSSDAESTNYNEIPKNGKSTKGYVHNSRNOATLNEKORPFSKG 336
DB 765 DKPPAGKHSSEKSSDSS-----SKLAKRKGEARDCD-----NKKLR----- 805
QY 337 KSGGLPFRSLDNEINEMDSFNGSPHENIT-----HGKHYVPHRONSTRNK 388
DB 806 -----LEKIKSSSSSSSHKSKXTKPSRPSQSSKKNLPPPVSSSSQK 854
QY 389 GMPQKGS-----WGSP-----HSNRFRSRRDDSSSSSSSSSE-----SDQ 430
DB 855 AKPALKSRBRADTCGQPPKASASTKSNHDSIIPQRRVKGKRSSEHKSSGD 912

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 1187 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-545-860D-28

Query Match

Best Local Similarity 20.6%; Score 136; DB 3; Length 1187;
Pred. No. 0.007;

Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;

QY 92 AKAHSKDKKKQORNS-----QAQSPVKSSTHRIQHNIDYLKLSKV 135

DB 530 SQEHSESKDPPKSSSKAPRAPAPHPGKRSCQKSPQDEPPQOTVGTQPK-----K 584

QY 136 KIPDFEGSGYTDLQERGDNDISPFSGDQPFKDIP---GKGE-----ATGPD 181

DB 585 PVKASAAAGSTSIQGEREPGLPYGSRDQTSKDKPKVTKGRPRAAASNEPKPAVPSS 644

QY 182 EKKDICTGFPAGPSAES-----THLDTKRGY-----NEIPREENGNTIGTRDE 227

DB 645 EKKHKSILPAPSKALSGPEPAKDNVEDRTEHPALVPLETSQGFPHSGSGSRTSGCQA 704

QY 228 TAKADAVDVLVGSNDIMGSTNFKELPGREGNRV-----DAGSQAHOQKVE 276

DB 705 VVVGQDSKDLPLPLRDTKLSPRLTPPQSLMVKITLTLRLIPQPKGSRQRAE 764

QY 277 FHYPAPEKREKGGSSDAESTVYNEIPKXGKSTRGVSHNRQATLNEKQRFPSKG 336

DB 765 DKQPPAGKHSEKSSDSS-----SKLAKRKGAERDCD-----NKXIR----- 805

QY 337 KSQGLPIPSRLDNEIKNEMDSFNGPSHENTIT-----HGKRYVYVPHRONSTENK 388

DB 806 -----LEKIKSQSSSSSSSHKESKTPSRPSOSSCKEMLPPIPVSSSSQKP 854

QY 389 GMPQCKGS-----WGRQF-----HSNRPFSSRRDDSSBSSDSSSSS---SDGD 430

DB 855 AKPALKRSREADTCGQDPPKASSTKSNHSDSIPKQRYVEGKSSSSSHKSSGSD 912

PCT-US94-04496-28

RESULT 6

Sequence 28, Application PC/TUS9404496

GENERAL INFORMATION:

APPLICANT: Croce, Carlo

TITLE OF INVENTION: Diagnostics, Therapeutics and Methods

TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias

TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/04496

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Deluca Esq., Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-1242

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 1187 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US94-04496-28

Query Match

Best Local Similarity 20.6%; Score 136; DB 5; Length 1187;
Pred. No. 0.007;

Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;

QY 92 AKAHSKDKKKQORNS-----QAQSPVKSSTHRIQHNIDYLKLSKV 135

DB 530 SQEHSESKDPPKSSSKAPRAPAPHPGKRSCQKSPQDEPPQOTVGTQPK-----K 584

QY 136 KIPDFEGSGYTDLQERGDNDISPFSGDQPFKDIP---GKGE-----ATGPD 181

DB 585 PVKASAAAGSTSIQGEREPGLPYGSRDQTSKDKPKVTKGRPRAAASNEPKPAVPSS 644

QY 182 EKKDICTGFPAGPSAES-----THLDTKRGY-----NEIPREENGNTIGTRDE 227

DB 645 EKKHKSILPAPSKALSGPEPAKDNVEDRTEHPALVPLETSQGFPHSGSGSRTSGCQA 704

QY 228 TAKADAVDVLVGSNDIMGSTNFKELPGREGNRV-----DAGSQAHOQKVE 276

DB 705 VVVGQDSKDLPLPLRDTKLSPRLTPPQSLMVKITLTLRLIPQPKGSRQRAE 764

QY 277 FHYPAPEKREKGGSSDAESTVYNEIPKXGKSTRGVSHNRQATLNEKQRFPSKG 336

DB 765 DKQPPAGKHSEKSSDSS-----SKLAKRKGAERDCD-----NKXIR----- 805

QY 337 KSQGLPIPSRLDNEIKNEMDSFNGPSHENTIT-----HGKRYVYVPHRONSTENK 388

DB 806 -----LEKIKSQSSSSSSSHKESKTPSRPSOSSCKEMLPPIPVSSSSQKP 854

QY 389 GMPQCKGS-----WGRQF-----HSNRPFSSRRDDSSBSSDSSSSS---SDGD 430

DB 855 AKPALKRSREADTCGQDPPKASSTKSNHSDSIPKQRYVEGKSSSSSHKSSGSD 912

US-08-320-559-26

RESULT 7

Sequence 26, Application US/08320559

Patent No. 5631135

GENERAL INFORMATION:

APPLICANT: Croce, Carlo

TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for

TITLE OF INVENTION: Detection and Treatment of Acute Leukemias

TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5631135

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/320,559

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Deluca Esq., Mark

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/062,443
 FILING DATE: 14 MAY 1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/971,094
 FILING DATE: 30-OCT-92
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/888,830
 FILING DATE: 27-MAY-92
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/805,093
 FILING DATE: 11-DEC-91
 ATTORNEY/AGENT INFORMATION:
 NAME: DeLuca, Mark
 REGISTRATION NUMBER: 33,229
 REFERENCE/DOCKET NUMBER: TUV-0855
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1210 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-320-559-26

Query Match 6.0%; Score 136; DB 1; Length 1210;
 Best Local Similarity 20.6%; Pred. No. 0.0072;
 Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;

92 AKASHKDKKKPKQDS-----QAQSPVSKSTRIQHNIDYLKLSKV 135
 553 SOHSESKDPPPKSSKAPAPAPAPHPGKSCQSPAQEPPOQVGTGKPK-----K 607
 136 KIPSDFGSGYTDIOERGNDISPFGDQPFKIP--GKGE-----ATGPD 181
 608 PVKASARAGSRISLOGEREPGLIPYGRDQTSKDKPKVKTGRPRAASNEPKPAVPSS 667
 182 EKGDIOTGAPGSEAS-----THLDTKKPGY-----NEIPRENGNTIGTRDE 227
 668 EKKKHKSSLPAPSKALSGEPKADVDRTPHFAVLPITSGQPHSGSGSRSGCRQA 727
 228 TAKEADAVVSLVEGSDNDMGSTNFKELPGREGNRV-----DAGSQNAHQKVE 276
 728 VVVGDSKDRPLPLRDTKLISPLRDTPPQSLMVKITLIDLSRIPQPEKSGRQKAE 787
 277 FHYPAPPEKEREKSSDAESTNNELPKNGKSTRGVDSHRNQAATLNEKQRFPSK 336
 788 DKQPPAGKHSSEKSSDS-----SKLAKRKGEAERDC-----NKKIR----- 828
 337 KSGGLPIPSGLDNEIKNEMDSFNGPSHENIT-----HGKHYVPHRQNNSTRNK 388
 829 -----LEKTEKQSSSSSSSHKESKTKSRPSQSSKEMLPPEPVSSSSQKP 877
 389 GMPQCKGS-----WGRQP-----HNNRFFSSKRRDSSSESSDSSGSSS---SDGD 430
 878 AKPALKSRREADTCGQDPKPSASSTKSNHXSIPKORAVEGKSSRSEHKSSGD 935

RESULT 8
 US-08-545-860D-26
 Sequence 26, Application US/08545860D
 Patent No. 6040140
 GENERAL INFORMATION:
 APPLICANT: Croce, Carlo
 APPLICANT: Canaan, Eli
 TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
 TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
 TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
 NUMBER OF SEQUENCES: 94
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
 ADDRESS: No. 6040140is
 STREET: One Liberty Place, 46th floor
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/545,860D
 FILING DATE: 07-MAR-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/04496
 FILING DATE: 22-APR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/10930
 FILING DATE: 09-DEC-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/327,392
 FILING DATE: 19-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/320,559
 FILING DATE: 11-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/062,443
 FILING DATE: 14-MAY-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/971,094
 FILING DATE: 30-OCT-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/888,839
 FILING DATE: 27-MAY-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/805,093
 FILING DATE: 11-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: DeLuca, Mark
 REGISTRATION NUMBER: 33,229
 REFERENCE/DOCKET NUMBER: TUV-1262
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1210 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-545-860D-26

Query Match 6.0%; Score 136; DB 3; Length 1210;
 Best Local Similarity 20.6%; Pred. No. 0.0072;
 Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;

92 AKASHKDKKKPKQDS-----QAQSPVSKSTRIQHNIDYLKLSKV 135
 553 SOHSESKDPPPKSSKAPAPAPAPHPGKSCQSPAQEPPOQVGTGKPK-----K 607
 136 KIPSDFGSGYTDIOERGNDISPFGDQPFKIP--GKGE-----ATGPD 181
 608 PVKASARAGSRISLOGEREPGLIPYGRDQTSKDKPKVKTGRPRAASNEPKPAVPSS 667
 182 EKGDIOTGAPGSEAS-----THLDTKKPGY-----NEIPRENGNTIGTRDE 227
 668 EKKKHKSSLPAPSKALSGEPKADVDRTPHFAVLPITSGQPHSGSGSRSGCRQA 727
 228 TAKEADAVVSLVEGSDNDMGSTNFKELPGREGNRV-----DAGSQNAHQKVE 276

DB 728 VVQEDSKRDLPLPLRDTKLLSPDRPQSLMVKITLDSLRIPOPGKSGRORAE 787
QY 277 FHYPAPSKERKKGSSDAASTYNNEIPKNGKSTKGVDSNRNQTLINEKORFPGK 336
DB 788 DKQPPAGKHSERKSSDSS-----SKLAKRKGEAREDC-----NKLR----- 828
QY 337 KSGGLPIPSRGIDNEIKEMDSFNQPSHENTIT-----HGKTYVPHRONNSTRNK 388
DB 829 -----LEKIKSGSSSSSSSHKESKTKPRSPSSQSKXEMLPPEVSSSSQKP 877
QY 389 GMPQKGS-----WGROP-----HNRKFRSSRRDDSSSSSSSSSE---SDGP 430
DB 878 AKPALKRSREADTGGDPPKASSTKSNHKOSSIPOKRVGKGSRSSSEHKSSGD 935

RESULT 9

PCT-US94-04496-26
Sequence 26, Application PC/TUS9404496
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the ALL-1
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/04496
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca Reg., Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1210 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-04496-26

Query Match 6.0%; Score 136; DB 5; Length 1210;
Best Local Similarity 20.6%; Pred. No. 0.0072;
Matches 86; Conservative 52; Mismatches 166; Indels 114; Gaps 14;

QY 92 AKAHSDKKKKPODS-----QAQKSPYKSKSTHICINIDYKHLKSVK 135
DB 553 SEHSSSKDPPSSSSKAPRAPEAPHPGKSCQKSPAQDPPQQTGVTQPKR---K 607
QY 136 KIPSPFEGSGYTDLQERDNDISPSGCGQPFKIDIP---GKGE-----ATGPD 181
DB 608 PVKASARASRTSLQGEREPGLLPYGSRGQTSKDKPKVTKGRPAAASNEPKAVPSS 667
QY 182 EGDIDTGAQPSSEAS-----THLDTKKPGY-----NEIPRENGANTIGTDE 227
DB 668 EKKGHKSLPAPPKALSGEPAPKDNVEDRTFHFALVPLTESQGPSPHSGSGSRISGCRQA 727

QY 228 TAKEADAVDVLVEGSDNDINGSTNFKELPGSEGNRV-----DAGQNAHQKVE 276
DB 728 VVQEDSKRDLPLPLRDTKLLSPDRPQSLMVKITLDSLRIPOPGKSGRORAE 787
QY 277 FHYPAPSKERKKGSSDAASTYNNEIPKNGKSTKGVDSNRNQTLINEKORFPGK 336
DB 788 DKQPPAGKHSERKSSDSS-----SKLAKRKGEAREDC-----NKLR----- 828
QY 337 KSGGLPIPSRGIDNEIKEMDSFNQPSHENTIT-----HGKTYVPHRONNSTRNK 388
DB 829 -----LEKIKSGSSSSSSSHKESKTKPRSPSSQSKXEMLPPEVSSSSQKP 877
QY 389 GMPQKGS-----WGROP-----HNRKFRSSRRDDSSSSSSSSSE---SDGP 430
DB 878 AKPALKRSREADTGGDPPKASSTKSNHKOSSIPOKRVGKGSRSSSEHKSSGD 935

RESULT 10

US-07-814-964-11
Sequence 11, Application US/07814964
Patent No. 5359047
GENERAL INFORMATION:
APPLICANT: Donahue, Brian A.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Bruhn, Suzanne L.
APPLICANT: Pil, Pieter M.
APPLICANT: Brown, Steven
APPLICANT: Kelleet, Patci
APPLICANT: Esselmann, John M.
TITLE OF INVENTION: DNA Structure Specific Recognition
TITLE OF INVENTION: Protein and Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/814,964
FILING DATE: 19911226
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/539,906
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4787A2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-9540
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 11
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Drosophila melanogaster
IMMEDIATE SOURCE:
CLONE: Drosophila ssRP (predicted)
FEATURE:
NAME/KEY: Domain
LOCATION: 458..507

MEDIUM TYPE: Floppy disk

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RESULT 12
US-08-328-809-6
Sequence 6, Application US/08328809
Patent No. 5705334

GENERAL INFORMATION:
APPLICANT: Lippard, Stephen J.
APPLICANT: Essigmann, John M.
APPLICANT: Donahue, Brian A.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Bruhn, Suzanne L.
APPLICANT: Pili, Pletcher M.
APPLICANT: Brown, Steven
APPLICANT: Kellelt, Patti
TITLE OF INVENTION: Uses For DNA Structure-Specific
TITLE OF INVENTION: Recognition Proteins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Patent Administrator, Testa, Hurwitz & Thibault
STREET: 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328, 809
FILING DATE:
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Fenton, Gillian M.
REGISTRATION NUMBER: 36, 508
REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Drosophila melanogaster

IMMEDIATE SOURCE:
CLONE: Drosophila SSrp (predicted)

FEATURE:
NAME/KEY: Domain
LOCATION: 458..507
OTHER INFORMATION: /label= Acidic

FEATURE:
NAME/KEY: Domain
LOCATION: 518..547
OTHER INFORMATION: /label= Basic I

FEATURE:
NAME/KEY: Domain
LOCATION: 547..620
OTHER INFORMATION: /label= HMG

FEATURE:
NAME/KEY: Domain
LOCATION: 632..649
OTHER INFORMATION: /label= Basic II
FEATURE:
NAME/KEY: Domain

LOCATION: 657..723
OTHER INFORMATION: /label= Mixed Charge
US-08-328-809-6

Query Match 5.9%; Score 135.5; DB 1; Length 723;
Best Local Similarity 23.2%; Pred. No. 0.0038;
Matches 81; Conservative 37; Mismatches 114; Indels 117; Gaps 18;

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QY 181 LEGKDIDTFAGPSEASTHLDTKKPGYNEIPERENGNTIGTRDEPAKADAVVSLV 240
Db 465 EDDDD---GDSESTDEDF-KPNESEDVAEYVSNEYSDSD---DSDAG--- 510
QY 241 EGSNDTGSTFKEIPREGNRVDAGSNALQKVEFHYPAPRKEKES----- 292
Db 511 -GGGSDGAKKK 562
QY 293 ---SDAAS-----TNYNEIPNGKSTRKGVDSNRQATLNEKPPSKGSGGL 341
Db 563 MMTNDTRESIKRENPGIKYTEIAKKGEMMKELKDKSKWDAKAKQRY----- 613
QY 342 PTPSRGLDNEIKNENDSRNGSHENITRGRKHYVPRKNNSTRNKMPPGKSGWGR-- 399
Db 614 -----HDEMRYKPPAGDSDSNEKG---GSKSKKRYT 642

RESULT 13
US-08-866-840-6
Sequence 6, Application US/08866840
Patent No. 6475791

GENERAL INFORMATION:
APPLICANT: Lippard, Stephen J.
APPLICANT: Essigmann, John M.
APPLICANT: Donahue, Brian A.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Bruhn, Suzanne L.
APPLICANT: Pili, Pletcher M.
APPLICANT: Brown, Steven
APPLICANT: Kellelt, Patti
TITLE OF INVENTION: Uses For DNA Structure-Specific
TITLE OF INVENTION: Recognition Proteins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: Patent Administrator, Testa, Hurwitz & Thibault
STREET: 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/866, 840
FILING DATE: 02-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fenton, Gillian M.
REGISTRATION NUMBER: 36, 508
REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 6:

TITLE OF INVENTION: Protein and Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11107
FILING DATE: 19921218
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/5519,906
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4787AAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 723 amino acids

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? TYPE: AMINO ACID
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? ORIGINAL SOURCE:
? ORGANISM: Drosophila melanogaster
? IMMEDIATE SOURCE:
? CLONE: Drosophila SSRP (predicted)
? FEATURE:
? NAME/KEY: Domain
? LOCATION: 458..507
? OTHER INFORMATION: /label= Acidic
? FEATURE:
? NAME/KEY: Domain
? LOCATION: 518..547
? OTHER INFORMATION: /label= Basic I
? FEATURE:
? NAME/KEY: Domain
? LOCATION: 547..620
? OTHER INFORMATION: /label= HMG-box
? FEATURE:
? NAME/KEY: Domain
? LOCATION: 632..649
? OTHER INFORMATION: /label= Basic II
? FEATURE:
? NAME/KEY: Domain
? LOCATION: 657..723
? OTHER INFORMATION: /label= Mixed Charge
PCT-US92-11107-11

Query Match          5.9%; Score 135.5; DB 5; Length 723;
Best Local Similarity 23.2%; Pred. No. 0.0038;
Matches      81; Conservative    37; Mismatches   14; Indels   117; Gaps    18

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DB      416 DYITQKKLHVSMMGR-----DKSGIKDY-DFGDS-----NNEEDAYLARUKAEAREKE 464

QY      181 LEKGDIQTGFAPGPSAESITHLDTKPKGYNELPEREENGANTIGTDETRAKEDAVDVSLV 240
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DB      465 EDDDD-----GDSDESSTDEDf-KPNENESPVAAEYDSNVSDSDD--DDASG--- 510

QY      241 EGSNDIMSGTNKELPGREGNRVDAAGSQAHGKVTEFHYPAPSKEREKES----- 292

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2004, 21:27:54 ; Search time 46 Seconds
(without alignments)
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Title: US-09-700-696C-2
Perfect score: 2276
Sequence: 1 UNKEXYSINKENTHNGLRMS.....RADDSESSSDSSSSSDSD 430

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1049977 seqs, 25855339 residues

Total number of hits satisfying chosen parameters: 1049977

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	2276	99.9	540	10	US-09-794-422-46
5	2276	99.9	556	10	US-09-794-422-8
6	2269	99.6	525	9	US-09-814-550-2
7	983.5	43.2	441	10	US-09-794-422-4
8	938.5	41.2	435	10	US-09-794-422-2
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10	246	10.8	47	9	US-09-812-485A-2
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16	214.5	9.4	45	9	US-09-812-485A-27	Sequence 27, Appl
17	198.5	8.7	41	9	US-09-812-485A-8	Sequence 8, Appl
18	190.5	8.4	40	9	US-09-812-485A-24	Sequence 24, Appl
19	189.5	8.3	40	9	US-09-812-485A-32	Sequence 32, Appl
20	182	8.0	37	9	US-09-812-485A-7	Sequence 7, Appl
21	180	7.9	38	9	US-09-812-485A-10	Sequence 10, Appl
22	163.5	7.2	35	9	US-09-812-485A-25	Sequence 25, Appl
23	157.5	6.9	35	9	US-09-812-485A-28	Sequence 28, Appl
24	153.5	6.7	33	9	US-09-812-485A-30	Sequence 30, Appl
25	152	6.7	1253	14	US-10-363-798-2	Sequence 2, Appl
26	150	6.6	32	9	US-09-812-485A-12	Sequence 12, Appl
27	148	6.5	1591	12	US-10-210-172-66	Sequence 66, Appl
28	148	6.5	1884	9	US-09-785-770A-17	Sequence 17, Appl
29	148	6.5	1907	9	US-09-785-770A-16	Sequence 16, Appl
30	148	6.5	1907	12	US-10-210-172-64	Sequence 64, Appl
31	146.5	6.4	33	9	US-09-812-485A-31	Sequence 31, Appl
32	146	6.4	2174	14	US-10-087-887-87	Sequence 87, Appl
33	145	6.4	940	15	US-10-108-260A-3781	Sequence 3781, Ap
34	144.5	6.3	665	10	US-09-820-443A-107	Sequence 107, Ap
35	142.5	6.3	31	9	US-09-812-485A-33	Sequence 33, Appl
36	142.5	6.3	31	9	US-09-812-485A-36	Sequence 36, Appl
37	140	6.1	772	14	US-10-153-668-302	Sequence 302, Ap
38	137.5	6.0	30	9	US-09-812-485A-26	Sequence 26, Appl
39	136	6.0	1210	14	US-10-205-823-264	Sequence 264, App
40	135	5.9	1742	12	US-10-615-383-4	Sequence 4, Appl
41	134.5	5.9	1115	13	US-10-153-373-2	Sequence 1, Appl
42	133.5	5.9	1462	14	US-10-287-218-17	Sequence 17, Appl
43	133	5.8	748	15	US-10-108-260A-3747	Sequence 3747, Ap
44	133	5.8	1069	12	US-10-424-599-259331	Sequence 259331,
45	132	5.8	1633	12	US-10-282-122A-70437	Sequence 70437, A

ALIGNMENTS

RESULT 1

US-09-794-422-34
; Sequence 34, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gomen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulin
; FILE REFERENCE: FC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 34
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-422-34

Query Match 99.8%; Score 2276; DB 10; Length 509;
Best Local Similarity 99.8%; Pred. No. 7.6e-173;
Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 UNKEXYSINKENTHNGLRMSIYKSGNKGFEDGDAISKLDQERYGALLRNNQHIM 60
DB 80 LNKEXYSINKENTHNGLRMSIYKSGNKGFEDGDAISKLDQERYGALLRNNQHIM 139
QY 61 GPVTAIKLGEENKENTPRVLTNIIPASVNTYAKSKDKKKKPPORDSOAKSPYKSGSTR 120
DB 140 GPVTAIKLGEENKENTPRVLTNIIPASVNTYAKSKDKKKKPPORDSOAKSPYKSGSTR 199
QY 121 IGHNIDVLKHLKSVKILPSPFEGSGYTDLQERDNDISPFSSGQGCFKDIIPKGEATCPD 180

Db 200 IQHNIDYKHLKSVKXKIPSDPFGSGYTDLQERGDNDISPFSGDGPFFKDI PGKEATGPD 259
Qy 181 LEGKDIQTGPAGPSEASTHLDTKKPGYNEIPEREENGNTIGTRDETAKADAVDVSLV 240
Db 260 LEGKDIQTGPAGPSEASTHLDTKKPGYNEIPEREENGNTIGTRDETAKADAVDVSLV 319
Qy 241 EGSNDIMGSTNFKELPQREGNVDAGSQNAHQKVEFHYPPAPSKKKEGSSDAEESTN 300
Db 320 EGSNDIMGSTNFKELPQREGNVDAGSQNAHQKVEFHYPPAPSKKKEGSSDAEESTN 379
Qy 301 YNEIPKNGKSTRKGVDSHNRNQATLNEKORFPKSGKSGQLPIPSRGLDNEIKNEMDSFN 360
Db 380 YNEIPKNGKSTRKGVDSHNRNQATLNEKORFPKSGKSGQLPIPSRGLDNEIKNEMDSFN 439
Qy 361 GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKSGWGRQPHSNRRFSSRRRDDSSSD 420
Db 440 GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKSGWGRQPHSNRRFSSRRRDDSSSD 499
Qy 421 SGSSSESDDG 430
Db 500 SGSSSESDDG 509

RESULT 2
US-09-794-422-6
; Sequence 6, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PCI0445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-422-6

Query Match 99.9%; Score 2276; DB 10; Length 525;
Best Local Similarity 99.8%; Pred. No. 8e-173; 0; Indels 0; Gaps 0;
Matches 429; Conservative 1; Mismatches 0

Qy 1 VNKEYSISNKENTHGLRMSIYPKSTGNKGFEDGDDAISKLHDQBEYGAALIRNNMQHIM 60
Db 96 LNKEYSISNKENTHGLRMSIYPKSTGNKGFEDGDDAISKLHDQBEYGAALIRNNMQHIM 155

Qy 61 GPVTAIKLGEENKENTPRNVLIIPASMYAKAHKSKKKKQKQDSQAKSPVKSKSTHR 120
Db 156 GPVTAIKLGEENKENTPRNVLIIPASMYAKAHKSKKKKQKQDSQAKSPVKSKSTHR 215

Qy 121 IQHNIDYKHLKSVKXKIPSDPFGSGYTDLQERGDNDISPFSGDGPFFKDI PGKEATGPD 180
Db 216 IQHNIDYKHLKSVKXKIPSDPFGSGYTDLQERGDNDISPFSGDGPFFKDI PGKEATGPD 275

Qy 181 LEGKDIQTGPAGPSEASTHLDTKKPGYNEIPEREENGNTIGTRDETAKADAVDVSLV 240
Db 276 LEGKDIQTGPAGPSEASTHLDTKKPGYNEIPEREENGNTIGTRDETAKADAVDVSLV 335

Qy 241 EGSNDIMGSTNFKELPQREGNVDAGSQNAHQKVEFHYPPAPSKKKEGSSDAEESTN 300
Db 336 EGSNDIMGSTNFKELPQREGNVDAGSQNAHQKVEFHYPPAPSKKKEGSSDAEESTN 395

Qy 301 YNEIPKNGKSTRKGVDSHNRNQATLNEKORFPKSGKSGQLPIPSRGLDNEIKNEMDSFN 360
Db 396 YNEIPKNGKSTRKGVDSHNRNQATLNEKORFPKSGKSGQLPIPSRGLDNEIKNEMDSFN 455

Qy 361 GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKSGWGRQPHSNRRFSSRRRDDSSSD 420
Db 456 GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKSGWGRQPHSNRRFSSRRRDDSSSD 515

Qy 421 SGSSSESDDG 430
Db 516 SGSSSESDDG 525

Qy 301 YNEIPKNGKSTRKGVDSHNRNQATLNEKORFPKSGKSGQLPIPSRGLDNEIKNEMDSFN 360
Db 396 YNEIPKNGKSTRKGVDSHNRNQATLNEKORFPKSGKSGQLPIPSRGLDNEIKNEMDSFN 455

Qy 361 GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKSGWGRQPHSNRRFSSRRRDDSSSD 420
Db 456 GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKSGWGRQPHSNRRFSSRRRDDSSSD 515

Qy 421 SGSSSESDDG 430
Db 516 SGSSSESDDG 525

RESULT 3
US-10-311-840-1
; Sequence 1, Application US/10311840
; Publication No. US20030175808A1
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tomofumi
; APPLICANT: YAMADA, Takao
; APPLICANT: MORIMOTO, Shigetomo
; TITLE OF INVENTION: No. US20030175808A1el Protein and its DNA
; FILE REFERENCE: 2738USOP
; CURRENT APPLICATION NUMBER: US/10/311,840
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: PCT/JP01/05263
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: JP 2000-191088
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 1
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Human
US-10-311-840-1

Query Match 99.9%; Score 2276; DB 14; Length 525;
Best Local Similarity 99.8%; Pred. No. 8e-173; 0; Indels 0; Gaps 0;
Matches 429; Conservative 1; Mismatches 0

Qy 1 VNKEYSISNKENTHGLRMSIYPKSTGNKGFEDGDDAISKLHDQBEYGAALIRNNMQHIM 60
Db 96 LNKEYSISNKENTHGLRMSIYPKSTGNKGFEDGDDAISKLHDQBEYGAALIRNNMQHIM 155

Qy 61 GPVTAIKLGEENKENTPRNVLIIPASMYAKAHKSKKKKQKQDSQAKSPVKSKSTHR 120
Db 156 GPVTAIKLGEENKENTPRNVLIIPASMYAKAHKSKKKKQKQDSQAKSPVKSKSTHR 215

Qy 121 IQHNIDYKHLKSVKXKIPSDPFGSGYTDLQERGDNDISPFSGDGPFFKDI PGKEATGPD 180
Db 216 IQHNIDYKHLKSVKXKIPSDPFGSGYTDLQERGDNDISPFSGDGPFFKDI PGKEATGPD 275

Qy 181 LEGKDIQTGPAGPSEASTHLDTKKPGYNEIPEREENGNTIGTRDETAKADAVDVSLV 240
Db 276 LEGKDIQTGPAGPSEASTHLDTKKPGYNEIPEREENGNTIGTRDETAKADAVDVSLV 335

Qy 241 EGSNDIMGSTNFKELPQREGNVDAGSQNAHQKVEFHYPPAPSKKKEGSSDAEESTN 300
Db 336 EGSNDIMGSTNFKELPQREGNVDAGSQNAHQKVEFHYPPAPSKKKEGSSDAEESTN 395

Qy 301 YNEIPKNGKSTRKGVDSHNRNQATLNEKORFPKSGKSGQLPIPSRGLDNEIKNEMDSFN 360
Db 396 YNEIPKNGKSTRKGVDSHNRNQATLNEKORFPKSGKSGQLPIPSRGLDNEIKNEMDSFN 455

Qy 361 GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKSGWGRQPHSNRRFSSRRRDDSSSD 420
Db 456 GPSHENIITHGRKYHYVPHRQNNSTRNKGMPQKSGWGRQPHSNRRFSSRRRDDSSSD 515

Qy 421 SGSSSESDDG 430
Db 516 SGSSSESDDG 525

```
RESULT 4
US-09-794-422-46
; Sequence 46, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 46
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-422-46

Query Match      99.9%; Score 2276; DB 10; Length 540;
Best Local Similarity 99.8%; Pred. No. 8.3e-173;
Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 VNKEYSISNKENTHNGLRMSIYPKSTGNKGFEDGDDAISKLHDQEYGAALIRNNQHIM 60
Db      111 LNKEYSISNKENTHNGLRMSIYPKSTGNKGFEDGDDAISKLHDQEYGAALIRNNQHIM 170
QY      61 GPVTAIKLGEENKENTPRNVLNIIIPASMYAKAHSKDKKKPQRSQAOKSPVKSKSTHR 120
Db      171 GPVTAIKLGEENKENTPRNVLNIIIPASMYAKAHSKDKKKPQRSQAOKSPVKSKSTHR 230
QY      121 IQHNIDYLKHLKSVKVKIPSDFEFGSGYTDLQERGDNDISPFSGDGGOPFKDIPKGGEATGPD 180
Db      231 IQHNIDYLKHLKSVKVKIPSDFEFGSGYTDLQERGDNDISPFSGDGGOPFKDIPKGGEATGPD 290
QY      181 LEGKDIQTGFAGPSEAEATHLDTKPGYNEIPIPERENGNTIGTRDETAKEADAVDVSLV 240
Db      291 LEGKDIQTGFAGPSEAEATHLDTKPGYNEIPIPERENGNTIGTRDETAKEADAVDVSLV 350
QY      241 EGSNDIMGSTNFKELPGRGNRVDAQSQNAHOGKVEFHYPPAPSKSKKEGSSDAEAESTN 300
Db      351 EGSNDIMGSTNFKELPGRGNRVDAQSQNAHOGKVEFHYPPAPSKSKKEGSSDAEAESTN 410
QY      301 YNEIPKNGKSTRKGVYDHSNRNQATLNEKQRPFPKSGKQGLPIPSRGLDNEIKNEMDSFN 360
Db      411 YNEIPKNGKSTRKGVYDHSNRNQATLNEKQRPFPKSGKQGLPIPSRGLDNEIKNEMDSFN 470
QY      361 GPSHENIITHGRKYHVPHRQNNSTNRKMGPOKSGWGRQPHSNRRFSSRRDDSSSD 420
Db      471 GPSHENIITHGRKYHVPHRQNNSTNRKMGPOKSGWGRQPHSNRRFSSRRDDSSSD 530
QY      421 SGSSSESDDGD 430
Db      531 SGSSSESDDGD 540

RESULT 5
US-09-794-422-8
; Sequence 8, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
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US-09-794-422-8
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 8
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-422-8

Query Match      99.9%; Score 2276; DB 10; Length 556;
Best Local Similarity 99.8%; Pred. No. 8.6e-173;
Matches 429; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 VNKEYSISNKENTHNGLRMSIYPKSTGNKGFEDGDDAISKLHDQEYGAALIRNNQHIM 60
Db      127 LNKEYSISNKENTHNGLRMSIYPKSTGNKGFEDGDDAISKLHDQEYGAALIRNNQHIM 186
QY      61 GPVTAIKLGEENKENTPRNVLNIIIPASMYAKAHSKDKKKPQRSQAOKSPVKSKSTHR 120
Db      187 GPVTAIKLGEENKENTPRNVLNIIIPASMYAKAHSKDKKKPQRSQAOKSPVKSKSTHR 246
QY      121 IQHNIDYLKHLKSVKVKIPSDFEFGSGYTDLQERGDNDISPFSGDGGOPFKDIPKGGEATGPD 180
Db      247 IQHNIDYLKHLKSVKVKIPSDFEFGSGYTDLQERGDNDISPFSGDGGOPFKDIPKGGEATGPD 306
QY      181 LEGKDIQTGFAGPSEAEATHLDTKPGYNEIPIPERENGNTIGTRDETAKEADAVDVSLV 240
Db      307 LEGKDIQTGFAGPSEAEATHLDTKPGYNEIPIPERENGNTIGTRDETAKEADAVDVSLV 366
QY      241 EGSNDIMGSTNFKELPGRGNRVDAQSQNAHOGKVEFHYPPAPSKSKKEGSSDAEAESTN 300
Db      367 EGSNDIMGSTNFKELPGRGNRVDAQSQNAHOGKVEFHYPPAPSKSKKEGSSDAEAESTN 426
QY      301 YNEIPKNGKSTRKGVYDHSNRNQATLNEKQRPFPKSGKQGLPIPSRGLDNEIKNEMDSFN 360
Db      427 YNEIPKNGKSTRKGVYDHSNRNQATLNEKQRPFPKSGKQGLPIPSRGLDNEIKNEMDSFN 486
QY      361 GPSHENIITHGRKYHVPHRQNNSTNRKMGPOKSGWGRQPHSNRRFSSRRDDSSSD 420
Db      487 GPSHENIITHGRKYHVPHRQNNSTNRKMGPOKSGWGRQPHSNRRFSSRRDDSSSD 546
QY      421 SGSSSESDDGD 430
Db      547 SGSSSESDDGD 556

RESULT 6
US-09-814-550-2
; Sequence 2, Application US/09814550
; Patent No. US20020102641A1
; GENERAL INFORMATION:
; APPLICANT: Schiavi, Susan
; APPLICANT: Madden, Stephen
; APPLICANT: Manavalan, Parthasarathy
; APPLICANT: Levine, Michael
; APPLICANT: Jan de Beur, Suzanne
; TITLE OF INVENTION: ONCOGENIC OSTEOCALCIN-RELATED GENE 1
; FILE REFERENCE: 5014US
; CURRENT APPLICATION NUMBER: US/09/814,550
; CURRENT FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 60/191,786
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 60/241,598
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 525
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-814-550-2

Query Match
Best Local Similarity 99.6%; Score 2269; DB 9; Length 525;
Matches 428; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNKEYSISNKNTHGLRMSIYPKSTGNKGFDDGDAISKLDHDEYGAALIRNMOMHIM 60
DB 96 LNKEYSISNKNTHGLRMSIYPKSTGNKGFDDGDAISKLDHDEYGAALIRNMOMHIM 155
QY 61 GPVTAIKLGEENKENTPRNVNIIIPASVNYAKAHSKDKKKPQDSDQAKSPVKSSTHR 120
DB 156 GPVTAIKLGEENKENTPRNVNIIIPASVNYAKAHSKDKKKPQDSDQAKSPVKSSTHR 215
QY 121 IOHNDYKHLKSVKVKIPSDFGSGYTDLOERGNDISPFSGDGPFPKDIIPKGEATGPD 180
DB 216 IOHNDYKHLKSVKVKIPSDFGSGYTDLOERGNDISPFSGDGPFPKDIIPKGEATGPD 275
QY 181 LEGKDIQTGFAGPSEASTHLDTKKPGYNEIIPEREENGNTIGTRDETAKEADAVDVSLV 240
DB 276 LEGKDIQTGFAGPSEASTHLDTKKPGYNEIIPEREENGNTIGTRDETAKEADAVDVSLV 335
QY 241 EGSNDIMGSTNFKELPGREGNVDAGSQNAHQGVFFHYPPAPSKKKEGSSDAESTN 300
DB 336 EGSNDIMGSTNFKELPGREGNVDAGSQNAHQGVFFHYPPAPSKKKEGSSDAESTN 395
QY 301 YNEIPKNGKSTRGKGVDSHNRNQATLNEKORPFSKGSQGLPIPSRGLDNEIKNEMDSFN 360
DB 396 YNEIPKNGKSTRGKGVDSHNRNQATLNEKORPFSKGSQGLPIPSRGLDNEIKNEMDSFN 455
QY 361 GSHENIITHGRKYHYVPHRQNNSTNRKGMPOKGSWGRQPHSNRRFRSSRDDSSSD 420
DB 456 GSHENIITHGRKYHYVPHRQNNSTNRKGMPOKGSWGRQPHSNRRFRSSRDDSSSD 515
QY 421 SGSSSESDDG 430
DB 516 SGSSSESDDG 525

RESULT 7
US-09-794-422-4
; Sequence 4, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-794-422-4

Query Match
Best Local Similarity 50.5%; Score 983.5; DB 10; Length 441;
Matches 217; Conservative 52; Mismatches 134; Indels 27; Gaps 8;

QY 6 SISKNTNTHGLRMSIYPKSTGNKGFDDGDAISKLDHDEYGAALIRNMOMHIMPVTA 65
DB 34 SCGNQDSIHKDLAASVYPTVDEGTEDGQALLHPGQDRYGAALLRNITQPVKSLVTG 93

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-814-550-2

Query Match
Best Local Similarity 99.5%; Score 2269; DB 9; Length 525;
Matches 428; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VNKEYSISNKNTHGLRMSIYPKSTGNKGFDDGDAISKLDHDEYGAALIRNMOMHIM 60
DB 96 LNKEYSISNKNTHGLRMSIYPKSTGNKGFDDGDAISKLDHDEYGAALIRNMOMHIM 155
QY 61 GPVTAIKLGEENKENTPRNVNIIIPASVNYAKAHSKDKKKPQDSDQAKSPVKSSTHR 120
DB 156 GPVTAIKLGEENKENTPRNVNIIIPASVNYAKAHSKDKKKPQDSDQAKSPVKSSTHR 215
QY 121 IOHNDYKHLKSVKVKIPSDFGSGYTDLOERGNDISPFSGDGPFPKDIIPKGEATGPD 180
DB 216 IOHNDYKHLKSVKVKIPSDFGSGYTDLOERGNDISPFSGDGPFPKDIIPKGEATGPD 275
QY 181 LEGKDIQTGFAGPSEASTHLDTKKPGYNEIIPEREENGNTIGTRDETAKEADAVDVSLV 240
DB 276 LEGKDIQTGFAGPSEASTHLDTKKPGYNEIIPEREENGNTIGTRDETAKEADAVDVSLV 335
QY 241 EGSNDIMGSTNFKELPGREGNVDAGSQNAHQGVFFHYPPAPSKKKEGSSDAESTN 300
DB 336 EGSNDIMGSTNFKELPGREGNVDAGSQNAHQGVFFHYPPAPSKKKEGSSDAESTN 395
QY 301 YNEIPKNGKSTRGKGVDSHNRNQATLNEKORPFSKGSQGLPIPSRGLDNEIKNEMDSFN 360
DB 396 YNEIPKNGKSTRGKGVDSHNRNQATLNEKORPFSKGSQGLPIPSRGLDNEIKNEMDSFN 455
QY 361 GSHENIITHGRKYHYVPHRQNNSTNRKGMPOKGSWGRQPHSNRRFRSSRDDSSSD 420
DB 456 GSHENIITHGRKYHYVPHRQNNSTNRKGMPOKGSWGRQPHSNRRFRSSRDDSSSD 515
QY 421 SGSSSESDDG 430
DB 516 SGSSSESDDG 525

RESULT 8
US-09-794-422-2
; Sequence 2, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-794-422-2

Query Match
Best Local Similarity 49.4%; Score 938.5; DB 10; Length 435;
Matches 211; Conservative 45; Mismatches 146; Indels 25; Gaps 8;

QY 9 NKENTNGLRMSIYPKSTGNKGFDDGDAISKLDHDEYGAALIRNMOMHIMPVTAIKL 68
DB 29 NQGNTH---LASVKEPFPVYKGTGGEDAPLHLLDNRQGAALLRNITQPVKSLVTGTEV 85
QY 69 LGSEENKENTPRNVNIIIPASVNYAKAHSKDKKKPQDSDQAKSPVKSSTHRIOHNDYL 128
DB 86 QSDRNKEKPKQSVLSVPTDVHNTNDYSEDNTENQQRDLNLSQSPGSKETPRARRSTHYL 145
QY 129 KHLKSVKVKIPSDFGSGYTDLOERGNDISPFSGDGPFPKDIIPKGEATGPDLE---GKD 185
DB 146 THLPQIRKILSDSDASPDLLVIRGNDVPPFSGDQGHFMHFDRCGAVGSPSSAGHP 205
QY 186 IOTGFAGPSEASTHLDTKKPGYNEIIPEREENGNTIGTRDETAKEADAVDVSLVSGSD 245

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Db 206 V-----SGSSNVEIVDPHTNGLSGSNEIPQRECHIGGAYATRGKTAQAGSADVSLVEGSNE 261
Qy 246 IMGSTNFXELPGRENRVDAGSQNAHQKVEFFHYPPAPSKKREKGGSDAAESTNYNEIP 305
Db 262 ITGSKFRELPGKGNRVDAASQNAHQKVEFFHYPPAPSKKREKGGREHTGKAGYNEIP 321
Qy 306 KNGKSTKGVVDHNRNQTALNEKQRPSPKSKQGLPIPSRGLDNEIKNEMDSTNGPSHE 365
Db 322 KSSKGGASKDAEESKGNQVTLTESQRPFGKGGQS-----SHSLGNEVKSEEDSSNSLSRE 377
Qy 366 NI-ITHGRKYHVPHRQNNSTRNKMPQKGSW-GRQPHSNRRSSRRRDDSSSSSSGS 423
Db 378 GIAIHRATSH-----PTNRGMSQRRGSWASRRRPHPRVSTQR-DSSSSSSSGS 428
Qy 424 SSESQGD 430
Db 429 SSESQGD 435

RESULT 9
US-09-812-485A-1
; Sequence 1, Application US/09812485A
; Publication No. US20020197267A1
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Yoshinari
; APPLICANT: Blacher, Russel
; APPLICANT: Yoneda, Toshiyuki
; TITLE OF INVENTION: Integrin Binding Motif Containing
; FILE REFERENCE: BEAR-006CIP
; CURRENT APPLICATION NUMBER: US/09/812,485A
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/641,034
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptidic compound
US-09-812-485A-1

Query Match 22.6%; Score 514; DB 9; Length 97;
Best Local Similarity 100.0%; Pred. No. 2e-33;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 105 DSOAQSPVKSKSTHRIQHNIDYLKHLKSVKXKIPSPDFEGSGYTDLOERGDNDISPFSGDG 164
Db 1 DSOAQSPVKSKSTHRIQHNIDYLKHLKSVKXKIPSPDFEGSGYTDLOERGDNDISPFSGDG 60

Qy 165 QPFPKIDIPGKGATGPDLGKDIQTGFPAGPSEASTHL 201
Db 61 QPFPKIDIPGKGATGPDLGKDIQTGFPAGPSEASTHL 97

RESULT 10
US-09-812-485A-2
; Sequence 2, Application US/09812485A
; Publication No. US20020197267A1
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Yoshinari
; APPLICANT: Blacher, Russel
; APPLICANT: Yoneda, Toshiyuki
; TITLE OF INVENTION: Integrin Binding Motif Containing
; FILE REFERENCE: BEAR-006CIP
; CURRENT APPLICATION NUMBER: US/09/812,485A
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/641,034
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 50
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptidic compound
US-09-812-485A-2

Query Match 10.8%; Score 246; DB 9; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.7e-12;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 AQSPVKSKSTHRIQHNIDYLKHLKSVKXKIPSPDFEGSGYTDLOERGD 154
Db 1 AQSPVKSKSTHRIQHNIDYLKHLKSVKXKIPSPDFEGSGYTDLOERGD 47

RESULT 11
US-09-812-485A-4
; Sequence 4, Application US/09812485A
; Publication No. US20020197267A1
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Yoshinari
; APPLICANT: Blacher, Russel
; APPLICANT: Yoneda, Toshiyuki
; TITLE OF INVENTION: Integrin Binding Motif Containing
; FILE REFERENCE: BEAR-006CIP
; CURRENT APPLICATION NUMBER: US/09/812,485A
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/641,034
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptidic compound
US-09-812-485A-4

Query Match 10.3%; Score 235.5; DB 9; Length 47;
Best Local Similarity 94.0%; Pred. No. 1.2e-11;
Matches 47; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 105 DSOAQSPVKSKSTHRIQHNIDYLKHLKSVKXKIPSPDFEGSGYTDLOERGD 154
Db 1 DSOAQSPVKSKSTHRIQHNIDYLKHLKSVKXKIPSPDFEGSGYTD---RGD 47

RESULT 12
US-09-812-485A-3
; Sequence 3, Application US/09812485A
; Publication No. US20020197267A1
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Yoshinari
; APPLICANT: Blacher, Russel
; APPLICANT: Yoneda, Toshiyuki
; TITLE OF INVENTION: Integrin Binding Motif Containing
; FILE REFERENCE: BEAR-006CIP
; CURRENT APPLICATION NUMBER: US/09/812,485A
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/641,034
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Artificial Sequence
```

FEATURE:
OTHER INFORMATION: peptidic compound
US-09-812-485A-3

Query Match 10.0%; Score 229; DB 9; Length 47;
Best Local Similarity 100.0%; Pred. No. 3.9e-11;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 AQSVPKSKSTHRIQHNIDYKHLKSKVKKIPSPDFGSGYTDLQE 151
Db 4 AQSVPKSKSTHRIQHNIDYKHLKSKVKKIPSPDFGSGYTDLQE 47

RESULT 13

US-09-812-485A-23
; Sequence 23, Application US/09912485A
; Publication No. US20020197267A1
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Yoshinari
; APPLICANT: Blacher, Russel
; APPLICANT: Yoneda, Toshiyuki
; TITLE OF INVENTION: Integrin Binding Motif Containing
; TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
; FILE REFERENCE: BEAR-006CIP
; CURRENT APPLICATION NUMBER: US/09/812,485A
; CURRENT FILING DATE: 2001-03-19
; PRIOR FILING DATE: 09/641,034
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptidic compound
US-09-812-485A-23

Query Match 9.6%; Score 218; DB 9; Length 40;
Best Local Similarity 100.0%; Pred. No. 2.3e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 152 RGNDISPFGDQPKDIPGKGATGPDLGKDIQTGFA 191
Db 1 RGNDISPFGDQPKDIPGKGATGPDLGKDIQTGFA 40

RESULT 14

US-09-812-485A-6
; Sequence 6, Application US/09812485A
; Publication No. US20020197267A1
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Yoshinari
; APPLICANT: Blacher, Russel
; APPLICANT: Yoneda, Toshiyuki
; TITLE OF INVENTION: Integrin Binding Motif Containing
; TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
; FILE REFERENCE: BEAR-006CIP
; CURRENT APPLICATION NUMBER: US/09/812,485A
; CURRENT FILING DATE: 2001-03-19
; PRIOR FILING DATE: 09/641,034
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptidic compound
US-09-812-485A-6

Query Match 9.5%; Score 216; DB 9; Length 44;

Best Local Similarity 88.0%; Pred. No. 3.8e-10;
Matches 44; Conservative 0; Mismatches 0; Indels 6; Gaps 1;
Qy 105 DSQAQSPVKSKSTHRIQHNIDYKHLKSKVKKIPSPDFGSGYTDLQERGD 154
Db 1 DSQAQSPVKSKSTHRIQHNIDYKHLKSKVKKIPSPDFGSG-----RGD 44

RESULT 15

US-09-812-485A-5
; Sequence 5, Application US/09812485A
; Publication No. US20020197267A1
; GENERAL INFORMATION:
; APPLICANT: Kumagai, Yoshinari
; APPLICANT: Blacher, Russel
; APPLICANT: Yoneda, Toshiyuki
; TITLE OF INVENTION: Integrin Binding Motif Containing
; TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
; FILE REFERENCE: BEAR-006CIP
; CURRENT APPLICATION NUMBER: US/09/812,485A
; CURRENT FILING DATE: 2001-03-19
; PRIOR FILING DATE: 09/641,034
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptidic compound
US-09-812-485A-5

Query Match 9.4%; Score 215; DB 9; Length 44;
Best Local Similarity 100.0%; Pred. No. 4.6e-10;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 SPVKSSTHRIQHNIDYKHLKSKVKKIPSPDFGSGYTDLQE 151
Db 4 SPVKSSTHRIQHNIDYKHLKSKVKKIPSPDFGSGYTDLQE 44

Search completed: March 24, 2004, 21:37:35
Job time : 47 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 29, 2004, 01:29:51 ; Search time 125 Seconds
(without alignments)
1909.031 Million cell updates/sec

Title: US-09-700-696C-2
Perfect score: 2279
Sequence: 1 VNKEYSINXKENTHGLRMS.....RRDSSSSSSGSSSSDGD 430

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Maximum Match 100%
Listing first 45 summaries

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV=xlh

-MODEL=frame_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09700696/runat_24032004_151402_1151/app_query.fasta_1.583
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPTXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09700696 @CGN 1.1 56 @runat_24032004_151402_1151 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT_DSFBLOCK=100 -LONGLOG
-NO_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:

- 1: /cgn2_6/ptodata/2/ina/5A-COMB.seq:
- 2: /cgn2_6/ptodata/2/ina/5B-COMB.seq:
- 3: /cgn2_6/ptodata/2/ina/6A-COMB.seq:
- 4: /cgn2_6/ptodata/2/ina/6B-COMB.seq:
- 5: /cgn2_6/ptodata/2/ina/PCTUS-COMB.seq:
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result; being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2279	100.0	1655	US-10-132-920B-1	Sequence 1, Appli
2	2276	99.9	2013	US-10-132-920B-26	Sequence 26, Appli
3	150	6.6	6755	US-08-931-999-4	Sequence 4, Appli
4	140	6.1	2690	US-08-524-757-11	Sequence 11, Appli
5	138.5	6.1	2384	US-07-814-964-10	Sequence 10, Appli
6	138.5	6.1	2384	US-08-258-443-10	Sequence 10, Appli
7	138.5	6.1	2384	US-08-328-809-5	Sequence 5, Appli
8	138.5	6.1	2384	US-08-866-840-5	Sequence 5, Appli
9	138.5	6.1	2384	PCT-US92-11107-10	Sequence 10, Appli
10	137	6.0	9370	US-08-320-559-27	Sequence 27, Appli
11	137	6.0	9370	US-08-545-860D-3	Sequence 27, Appli
12	137	6.0	9370	PCT-US94-04496-27	Sequence 27, Appli

13	137	6.0	9391	1	US-08-320-559-25	Sequence 25, Appli
14	137	6.0	9391	3	US-08-545-860D-25	Sequence 25, Appli
15	137	6.0	9391	5	PCT-US94-04496-25	Sequence 25, Appli
16	135	5.9	5406	4	US-09-386-962C-1	Sequence 1, Appli
17	134.5	5.9	4084	2	US-08-568-459A-1	Sequence 1, Appli
18	134.5	5.9	4084	2	US-08-487-826B-1	Sequence 1, Appli
19	134.5	5.9	4084	6	US-09-210-288-1	Sequence 1, Appli
20	134.5	5.9	4084	6	US-09-210-288-1	Sequence 1, Appli
21	129	5.7	3157	4	US-09-976-594-374	Patent No. 5198347
22	129	5.7	3157	6	US-09-976-594-374	Patent No. 5198347
23	127.5	5.6	3707	1	US-08-118-101A-1	Sequence 1, Appli
24	127	5.6	2695	4	US-09-706-197-3	Sequence 3, Appli
25	126.5	5.6	4215	4	US-09-620-312D-295	Sequence 295, Appli
26	126.5	5.6	1393	5	PCT-US93-07261-12	Sequence 12, Appli
27	126.5	5.6	3773	3	US-09-130-242-1	Sequence 1, Appli
28	125.5	5.5	3825	3	US-09-208-742-3	Sequence 3, Appli
29	125.5	5.5	5173	4	US-08-801-308-2	Sequence 2, Appli
30	124.5	5.5	3552	4	US-09-134-001C-693	Sequence 693, Appli
31	123	5.4	1503	3	US-08-999-774A-11	Sequence 11, Appli
32	123	5.4	3534	4	US-09-134-001C-2269	Sequence 2269, Appli
33	123	5.4	4766	5	PCT-US93-07261-10	Sequence 10, Appli
34	123	5.4	6775	4	US-09-620-312D-289	Sequence 289, Appli
35	122.5	5.4	3347	4	US-09-702-705-318	Sequence 318, Appli
36	122.5	5.4	3347	4	US-09-736-457-318	Sequence 318, Appli
37	122.5	5.4	3347	4	US-09-614-124B-318	Sequence 318, Appli
38	122.5	5.4	3347	4	US-09-671-325-318	Sequence 318, Appli
39	122.5	5.4	3347	4	US-09-589-184-318	Sequence 318, Appli
40	122	5.4	2073	4	US-09-134-001C-1731	Sequence 1731, Appli
41	122	5.4	43280	2	US-08-804-227C-1	Sequence 1, Appli
42	121	5.3	2004	1	US-08-471-033-18	Sequence 18, Appli
43	121	5.3	2004	2	US-08-471-044-18	Sequence 18, Appli
44	121	5.3	2004	2	US-08-463-483A-18	Sequence 18, Appli
45	121	5.3	2004	2	US-08-471-046A-18	Sequence 18, Appli

ALIGNMENTS

RESULT 1
US-10-132-920B-1
; Sequence 1, Application US/10132920B
; Patent No. 6673900
; GENERAL INFORMATION:
; APPLICANT: Rowe, Peter
; TITLE OF INVENTION: A Polypeptide Hormone-Phosphatonin
; FILE REFERENCE: BEAR-005CON
; CURRENT APPLICATION NUMBER: US/10/132,920B
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 09/434,185
; PRIOR FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1655
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-132-920B-1

Alignment Scores:
Pred. No.: 6.2e-213 Length: 1655
Score: 2279.00 Matches: 430
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-700-696C-2 (1-430) x US-10-132-920B-1 (1-1655)

QY 1 ValAsnIysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSer 20
DB 1 GTGAATTAAGAAATATAGTATCATCAGTACAAAGAGAACTACCAATGCGCTGAGGATGCA 60
QY 21 IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLys 40

Db 839 AGTGGGACGCGCAACCTTTAAGGACATTCCTGGTAAGGAGAGCTACTGTCTCTGAC 998
Qy 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
Db 899 CTAGAAGGCAAGATATTCACACAGGGTTTCAGGCGCAAGTGAAGCTGAGAGTACTCAT 958
Qy 201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyLys 220
Db 959 CTTGACACAAAAAGCCAGGTATATGATGATCCAGAGAGAGAGAAATGTGGAAT 1018
Qy 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuVal 240
Db 1019 ACCATTGGACTAGGATGAACCTCGAAGAGGACAGATGCTGTGATGTCAGCCITGTA 1078
Qy 241 GluGlySerAsnAspIleMetGlySerThrAsnPhelLysGluLeuProGlyArgGluGly 250
Db 1079 GAGGCGACGACGATATCATGGGTAGTACCAATTTTAAGGAGTCCCTCGAAGAGAGGA 1138
Qy 261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrPro 280
Db 1139 AACAGATGGATGCTGGCAGCCAAATGCTCACCAGAGGAGTTGATGTTTCATTACCT 1198
Qy 281 ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn 300
Db 1199 CCGTACCCCTCAAAAGAGAAAAAGAAAGAGAGGAGTGTGATGAGCTGAAGTACCAAC 1258
Qy 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
Db 1259 TATAATGAATTCCTAAATAATGGCAAGGCGAGTACCAGAAAGGTTGATCATCTTAAT 1318
Qy 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
Db 1319 AGGAACCAAGCAACCTTAATCAAAAAACAAAGGTTCTAGTAAGGCGCAAAAGTCAGGC 1378
Qy 341 LeuProIleProSerArgGlyLeuAspAsnGluLysLysGluMetAspSerPheAsn 360
Db 1379 CTGCCATCTCTCTCGGGTCTTGATATGAATCAAAATCAAAACGAAATGGATTCCTTAAT 1438
Qy 361 GlyProSerHisGluAsnIleThrHisGlyArgLysTyrHisTyrValProHisArg 380
Db 1439 GGCCCATCATGAGATATATATAACATATGAGCAAAATATATATATGATACCCACAGA 1498
Qy 381 GlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTyrGlyArgGln 400
Db 1499 CAAATAATCTTACACGGAATAAGGGTATGCCAAGGGAAGGCTCTGGGGGTAGCAA 1558
Qy 401 ProHisSerAsnArgArgPheSerSerArgArgAspAspSerSerGluSerSerAsp 420
Db 1559 CCCCATTCCACAGAGAGGTTTATGTTCCGTAGAGGAGTACAGTAGTGTCTCATCTGAC 1618
Qy 421 SerGlySerSerSerGluSerAspGlyAsp 430
Db 1619 AGTGGCAGTTCAAGTGAGAGCGATGCTGAC 1648

RESULT 3

US-08-931-999-4
; Sequence 4, Application US/08931999
; Patent No. 6043219
; GENERAL INFORMATION:
; APPLICANT: Iandolo, John J.
; APPLICANT: Crutcher, Scott S.
; TITLE OF INVENTION: Broad Spectrum Chemotherapeutic Peptide
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hovey, Williams, Timmons & Collins
; STREET: 2405 Grand Boulevard, Suite 400
; CITY: Kansas City
; STATE: Missouri
; COUNTRY: U.S.A.
; ZIP: 64108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931.999
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/710.561
FILING DATE: 19-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26,262
REFERENCE/DOCKET NUMBER: 25043-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 6755 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Staphylococcus aureus
STRAIN: UT0007
US-08-931-999-4

Alignment Scores:
Pred. No.: 0.00272 Length: 6755
Score: 150.00 Matches: 104
Percent Similarity: 31.05% Conservative: 59
Best Local Similarity: 19.81% Mismatches: 201
Query Match: 6.58% Indels: 162
Gaps: 20

US-09-700-696C-2 (1-430) x US-08-931-999-4 (1-6755)

Qy 2 AsnLysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSerIle 21
Db 4164 AACCAAAACAAACAGAGGGAAGCAAGCAACCCACCCACACGACAGAGGAA----- 4217
Qy 22 TyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLysLeu 41
Db 4218 -----AAGCAAAACGGCGGAAA-----AACGCCAAAAAAACAAACAA 4259
Qy 42 HisAspGlnGlu----- 45
Db 4260 CACAAGAGAGAAAAAGGCCACCGCAAAACAGCGCAAAACCCCGAGAAAAACAAAA 4319
Qy 46 ---GluTyrGlyAlaAlaLeuIleArgAsnMetGlnHisIleMetGlyProValThr 64
Db 4320 GGAIAAAAGCGAAAAAAGACACAAAGCAACAAAGAAAGAAAGAAAGCGGAAAAA 4379
Qy 65 AlaIleLysLeuLeuGlyGluGluAsnLysGluAsnThrProArgAsnValLeuAsnIle 84
Db 4380 AGAAGAAAA-----AAAAGCAAAACAGAGAGACCCCAACAAACACCAACAAAAACA 4433
Qy 85 IleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLysLysProGlnArg 104
Db 4434 CAAGGACGACAGGAAAAAGCGAGAACCCAGAAAAAAGGAAAAAAGGAAAAAAG 4493
Qy 105 AspSerGlnAlaGln-----Lys 110
Db 4494 GAAAGCAAAACCAAGACGAGGAGGAAACACACAAAAAGCGCGGAGCGGAGAAAAA 4553
Qy 111 SerProValLys-----SerLysSerThrHisArgIleGlnHisAsn 124
Db 4554 ACACCCCGAAAAAACAACAAAAAGACACACAAAAACCAACCCCAAGAGAGAGAAAC 4613
Qy 125 IleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAspPheGluGlySer 144

Db 767 ----- 767
Qy 83 AsnIlelleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLysLysPro 102
Db 768 ----- 768
Qy 103 GlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArgIleGln 122
Db 798 GATGCCAAGAGTGATGAGAACGGCTCTGTGTGTGAGCAGAGAGAAATCACAC----- 848
Qy 123 HisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAspPheGlu 142
Db 849 ----- 849
Qy 143 GlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGly 162
Db 864 ----- 864
Qy 163 AspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAspLeuGlu 182
Db 891 GACAATGCAAGGAGAAACCG---CCCTCTAGTGGCTAAAGAAAGAGAGAGAGAGAG 947
Qy 183 GlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSer---ThrHisLeu 201
Db 948 GCGACGAGCTGAGACAGAGAGTGTTCCTCTCCCTCAGAGGCGCTTCAGACAAACCACTG 1007
Qy 202 AspThrLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThr 221
Db 1008 ----- 1008
Qy 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValSerLeuValGlu 241
Db 1044 ----- 1044
Qy 242 GlySerAsnAspIleMet-----GlySerThrAsnPheLysGluLeu 255
Db 1089 GGAGCAGGAGACCTTGTCCCAAGGTAAAGAGAGGGTCTTAAACACTTAAAGACTTCA 1148
Qy 256 ProGlyArgGluGlyAsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysVal 275
Db 1149 GAAGGAAAGTCAAAACTAATTTGGTAGAAGAGTCACTGGGCTCC---CTCCCTAAAGTT 1205
Qy 276 ----- 280
Db 1206 GAGGAGACATATGAGGATGAATTCGAGCAGCCCAACCATCTCTTTGAATCTTACCTC 1265
Qy 281 ----- 281
Db 1266 AGCTATGACCCCGCGAGAGAAAGAAAGATTTGTAAGAACT---TCAGCCACGCA 1322
Qy 299 ThrAsnTyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHis 318
Db 1323 CTGGAGATAAAGGACTTAAAAAATGACTCTAAAGCACTGGTAAAGAACTTGGACTCA 1382
Qy 319 SerAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSer 338
Db 1383 GTTCAGAAATTATCCCAAGGTGAACAAACCAAGTCAGAGAACCCGCTGGAGCTGATT 1442
Qy 339 GlnGlyLeu----- 341
Db 1443 GCCAAGCTGAGAAAGGTGCTGATGTGTGCCAGTGTTCGACAGCTCCCGTTACCCGCG 1502
Qy 342 ----- 342
Db 1503 ATACAGCCCAATTACCGTCCACTGCTTCCCTGAGCTGATATCTCTCTTCCAGCAAAAG 1562
Qy 356 MetAspSerPheAsnGlyProSerHisGluAsn----- 366
Db 1563 CGAAAGCGTCTCTTCCACCCAGGAGAGAGAGAGCTGGATTCTTGGGCGCAGATG 1622
Qy 367 ----- 378
Db 1623 AATTCCAAGATGCGAGGTGATTCTGTGTTCCAAAGTGTGCCTATCTCCCTAAATGATGACC 1682

QY 379 ---HisArgGln 381
Db 1683 TTGCACCAAGCAA 1694

RESULT 5
US-07-814-964-10
; Sequence 10, Application US/07814964
; Patent No. 5359047
; GENERAL INFORMATION:
; APPLICANT: Donahue, Brian A.
; APPLICANT: Toney, Jeffrey H.
; APPLICANT: Bruhn, Suzanne L.
; APPLICANT: Pil, Pieter M.
; APPLICANT: Brown, Steven
; APPLICANT: Kellett, Patti
; APPLICANT: Essigmann, John M.
; APPLICANT: Lippard, Stephen J.
; TITLE OF INVENTION: DNA Structure Specific Recognition
; TITLE OF INVENTION: Protein and Uses Therefor
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: 2 Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/814,964
; FILING DATE: 19911226
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/539,906
; FILING DATE: 18-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: MIT-4787AAA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2384 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster
; IMMEDIATE SOURCE:
; CLONE: Drosophila SSRP - composite sequence
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 2
; MAP POSITION: 60A 1-4
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 123..2291
US-07-814-964-10

Alignment Scores:
Pred. No.: 0.000795
Score: 138.50
Percent Similarity: 31.91%
Best Local Similarity: 21.20%
Query Match: 6.08%
Db: 1
Length: 2384
Matches: 99
Conservative: 50
Mismatch: 136
Indels: 182
Gaps: 23

US-09-700-696C-2 (1-430) x US-07-814-964-10 (1-2384)

QY 16 GlyLeuArgMetSerIleTyrProLysSerThrGly-AsnLysGlyPheGluAspGlyAs 35
Db 1187 GGAGCGAGGATTCATCTATATCCACAGCCACCGCTGCATATCGCTTTGAGGAG-----1241
QY 35 pAspAlaIleSerLysLeuHisAspGlnGluGluTyrGlyAla-----49
Db 1242 -----ATTAGTTCGTGAACACTTTCGCCGAGCGCGGATCCACCGCATCTTCGACTT 1294
QY 50 -----AlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAlaIleLysLe 68
Db 1295 CGAAGTGCAGCTCAAGAGCGAAGCTGTTACATCTTCTCTCCATC-----1340
QY 68 uLeuGlyGluGlnAsnLysGluAsnThrProArgAsnValLeuAsnIleIleProAlaSe 88
Db 1341 -----GAGAAGGAGGAG-----1352
QY 88 rMetAsnTyrAlaLysAlaHisSerLysAspLysLysProGlnArgAspSerGlnAl 108
Db 1353 -----TATGCCAAGCTC-----1364
QY 108 aGlnLysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLe 128
Db 1365 -----TTGCACTACAT 1375
QY 128 uLys-----HisLeuSerLysValLysLysIleProSerAspPheGluGlySe 144
Db 1376 CACACAGAGAGATTCATGTGTCAGCAACATGGCGAAG-----GACAAGAG 1420
QY 144 rGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspLysSerProPheSerGlyAspGl 164
Db 1421 CGGCTACAGAGCGTG-----GACTTGGTGATTCGAGC-----AACGAGAA 1462
QY 164 yGlnProPheLysAspIleProGly-----LysGlyGluAlaThrGlyProAspLeuGluGl 183
Db 1463 CGAACCAGATGCTATCGCTCGCTCAGGCTGAGCGGAGGAGGAGGAGGAGCA 1522
QY 183 yAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspTh 203
Db 1523 CGACGAT-----GGCGACTCGATGAAGAGTCCACGGATGAGGACTT 1564
QY 203 rLysLysProGlyTyrAsnGluIleProGluArgGluAsnGlyGlyAsnThrIleGl 223
Db 1565 C---AAGCCCAACGAGACGAGTCCGATGTGCGCGAGGAGTATGACGCAACGTCGAGAG 1621
QY 223 yThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlySe 243
Db 1622 TGATTCGAGCAT-----GACAGCGATGCTAGTGGC-----GGCGG 1657
QY 243 rAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsnArgVa 263
Db 1658 AGCGCAGCGAGCGCGCCCAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAAA 1717
QY 263 lAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrProAlaPr 283
Db 1718 CGAGAAAAACACAG 1756
QY 283 oSerLysGluLysArgLysGluGlySer-----292
Db 1757 CTCGAAG 1816
QY 293 -----SerAspAlaAlaGluSer-----ThrAsnTyrAsnGluI 304
Db 1817 GCTGAACGACGCGCGAGAGCATCAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1876
QY 304 eProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAl 324
Db 1877 CGCCAAG 1936
QY 324 aThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGlyLeuProIlePr 344

1937 GCGCGCAAGCAAGCAAGCGCTAC-----1961
QY 344 oSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsnGlyProSerHi 364
Db 1961 -----1961
QY 364 sGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArgGlnAsnAsnSe 384
Db 1962 -----CACGACGAGATCGCAACTACAAAGCTGAAGCGGGGGTGACAG 2005
QY 384 rThrArgAsnLysGlyMetProGlnGlyLysGlySerTrpGlyArg-----GlnProHi 402
Db 2006 CGACACAGAGAGAGGGT-----GGAAAGTCTCCAAAGAGCCCAAGACGAGCCTTC 2056
QY 402 sSerAsnArgArg-----PheSerSerArgArg-----ArgAs 413
Db 2057 TCATCCAAAGAGGGAATACCTCGGCGAGCGCTTCAAGAGCAAGGAGTACATTTCCGA 2116
QY 413 pAspSerSerGluSerSerAspSerGlySerSerGlu-----426
Db 2117 CGACGACTCCACGCTCCGACGACGAGAGAGCAACGAGCCTGCCAAGAGAGAGCA 2176
QY 427 -----SerAspGlyAsp 430
Db 2177 GCGCGCGCTCCGAGCGGAT 2195

RESULT 6
US-08-258-442-10
Sequence 10, Application US/08258442
Patent No. 5670621
GENERAL INFORMATION:
APPLICANT: Donahue, Brian A.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Bruhn, Suzanne L.
APPLICANT: Pil, Pieter M.
APPLICANT: Brown, Steven
APPLICANT: Keillett, Patti
APPLICANT: Essigmann, John M.
APPLICANT: Lipard, Stephen J.
TITLE OF INVENTION: DNA Structure Specific Recognition
TITLE OF INVENTION: Protein and Uses Therefor
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,442
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/539,906
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4787AAA
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 2384 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

```

; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Drosophila melanogaster
; IMMEDIATE SOURCE:
; CLONE: Drosophila SRP - composite sequence
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 2
; MAP POSITION: 60A 1-4
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 123..2291
US-08-258-442-10

Alignment Scores:
Pred. No.: 0.000795 Length: 2384
Score: 138.50 Matches: 99
Percent Similarity: 31.91% Conservative: 50
Best Local Similarity: 21.20% Mismatches: 136
Query Match: 6.08% Indels: 182
DB: 1 Gaps: 23

US-09-700-696C-2 (1-430) x US-08-258-442-10 (1-2384)
QY 16 GlyLeuArgMetSerIleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAs 35
DB 1187 GGAGCGAGATTCATCTATATCCACAGCCCGCTGCATATCCGCTTGAGGAG-----1241
QY 35 PAspAlaIleSerLysLeuHisAspGlnGluGluTyrGlyAla-----49
DB 1242 -----ATTAGTCTGTGAACCTTTGCCCGCAGCGCGGATCCACGGCATCTTCGACTT 1294
QY 50 ----AlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAlaIleLysLe 68
DB 1295 CGAAGTGGCTCAAGAACGGACTGTTTCATCTCTCTCCATC-----1340
QY 68 uLeuGlyGluGlnAsnLysGluAsnThrProArgAsnValLeuAsnIleProAlaSe 88
DB 1341 -----GAGAAGGAGGAG-----1352
QY 88 rMetAsnTyrAlaLysAlaHisSerLysAspLysLysProGlnArgAspSerGlnAl 108
DB 1353 -----TATGCCAAGCTC-----1364
QY 108 aGlnLysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLe 128
DB 1365 -----TTGCACTACAT 1375
QY 128 uLys-----HisLeuSerLysValLysLysIleProSerAspPheGluGlySe 144
DB 1376 CACACAGAGAAGTTGCATGTGACGACATGGGCAAG-----GACAAGAG 1420
QY 144 rGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGl 164
DB 1421 CGGCTACAGGAGGTG--GACTTGTGTATTCGGAC-----AACGAGAA 1462
QY 164 yGlnProPheLysAspIleProGly--LysGlyGluAlaThrGlyProAspLeuGluGl 183
DB 1463 CGAACCATGATGCTCTATCTGCTCGCTCAAGCTGAGCGCGGAGGAGGAGGAGCA 1522
QY 183 yLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspTh 203
DB 1523 CGACGAT-----GGCGATCGGATGAGAGTCCACGGATGAGGACTT 1564
QY 203 rLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIleGl 223
DB 1565 C---AAGCCCAACGAGAACGATGTCGATGTGGCCGAGGAGTATGACAGCAACGTGGAGAG 1621
QY 223 yThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlySe 243
DB 1622 TGATTCGAGCAT-----GACAGCGATGATAGTGGC-----GGCGG 1657
QY 243 rAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsnArgVa 263

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1658 AGCGACACGCGACGCGCCCAAGAAAAGAGAGAGAGTCCCGAAGAAAGAAA 1717

263 lAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrProProAlaPr 283

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283 oSerLysGluLysArgLysGluGlySer-----292

1757 CTCCAAGAAAGAAAGAGACTCTGGCAAAACCCNAGCGCGCCACCACGGCTTTCATGCTCTG 1816

293 ----SerAspAlaAlaGluSer-----ThrAsnTyrAsnGluI 304

1817 GCTGAACGACACGCGGAGAGCATCAAGAGGGAATCCGGCATAAAGGTTTACCGAGAT 1876

304 eProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAl 324

1877 CGCCAAGAGGCGCGGAGATGTGAAGAGAGTGAAGACAAAGTCCAAGTGGGAGATGC 1936

324 aThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGlyLeuProIlePr 344

1937 GCGGCGCAAGGACACGACGCTAC-----1961

344 oSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsnGlyProSerHi 364

1961 -----1961

364 sGluAsnIleThrHisGlyArgLysTyrHisTyrValProHisArgGlnAsnAsnSe 384

1962 -----CACGACGAGATGCGCAACTACAGCTGAAGCGGCGGTGACAG 2005

384 rThrArgAsnLysGlyMetProGlnGlyLysGlySerThrGlyArg-----GlnProHi 402

2006 CGACAACGAGAGAGGT-----GGAAGTCTCTCAAGACCGCAACGAGCGCTTC 2056

402 sSerAsnArgArg-----PheSerSerArgArg-----ArgAs 413

2057 TCATCCAGAGAGCGAATACCTCGGCGAGCGCTTCAAGACGAGGATACATTTCCGA 2116

413 pAspSerSerGluSerSerAspSerGlySerSerSerGlu-----426

2117 CGACGACTCCACGAGCTCCGACGACGAGAGACACGACGCTGCCAAGAGAGAGCA 2176

427 -----SerAspGlyAsp 430

2177 GCGCCCATCCGACGCGCAT 2195

RESULT 7

US-08-328-809-5

Sequence 5, Application US/08328809

Patent No. 5705334

GENERAL INFORMATION:

APPLICANT: Lippard, Stephen J.

APPLICANT: Essigmann, John M.

APPLICANT: Donahue, Brian A.

APPLICANT: Toney, Jeffrey H.

APPLICANT: Bruhn, Suzanne L.

APPLICANT: Pil, Pieter M.

APPLICANT: Brown, Steven

APPLICANT: Kellert, Patti

TITLE OF INVENTION: Uses For DNA Structure-Specific

TITLE OF INVENTION: Recognition Proteins

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Patent Administrator, Testa, Hurwitz & Thibault

STREET: 53 State Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.125
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/328,809

FILING DATE:
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Fenton, Gillian M.

REGISTRATION NUMBER: 36,508

REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-248-7000

TELEFAX: 617-248-7100

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 2384 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: Drosophila melanogaster

IMMEDIATE SOURCE:

CLONE: Drosophila SSRP - composite sequence

POSITION IN GENOME:

CHROMOSOME/SEGMENT: 2

MAP POSITION: 60A 1-4

FEATURE:

NAME/KEY: CDS

LOCATION: 123...2291

US-08-328-809-5

Alignment Scores:

Pred. No.: 0.000795

Score: 138.50

Percent Similarity: 31.91%

Best Local Similarity: 21.20%

Query Match: 6.08%

DB: 1

US-09-700-696C-2 (1-430) x US-08-328-809-5 (1-2384)

16 GlyLeuArgMetSerLeuThrProLysSerThrGlyAsnLysGlyPheGluAspGlyAs 35

1187 GGAGCGAGGATTCATATATCCACAGCCCGCTGCATATCCGCTTTGAGGAG----- 1241

35 pAspAlaIleSerLysLeuHisAspGlnGluGlyAla----- 49

1242 -----ATTAGTTCTGTGAACCTTCCCGCAGCGCGGATCCACGCGATCTTCGACTT 1294

50 ----AlaLeuIleArgAsnMetGlnHisIleMetGlyProValThrAlaIleLysLe 68

1295 CGAAGTGACGCTCAAGACGGAACCTTTCACATCTTCTCCTCCATC----- 1340

68 uLeuGlyGluGluAsnLysGluAsnThrProArgAsnValLeuAsnIleProAlaSe 88

1341 -----GACAGCAGGAG----- 1352

88 rMetAsnTyrAlaLysAlaHisSerLysAspLysLysProGlnArgAspSerGlnAl 108

1353 -----TATGCCAAGCTC----- 1364

108 aGlnLysSerProValLysSerLysThrHisArgIleGlnHisAsnIleAspTyrLe 128

1365 -----TTGACTATCAT 1375

128 uLys-----HisLeuSerLysValLysLysIleProSerAspPheGluGlySe 144

1376 CACACAGAGAAGTTCATATCCACAGCAACATGGCGAAG-----CACACAGAG 1420

144 rGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGl 164

1421 CGGCTACAGGACGTG---GACTTTGTGTATTCCGAC-----AACGAGAA 1462

164 yGlnProPheLysAspIleProGly---LysGlyGluAlaThrGlyProAspLeuGluGl 183
 1463 CGAACCCAGATGCTATCTGCTCGCTCAAGCTCAGCGGAGGAAAGAGGAGGAGGACGA 1522
 183 yLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspTh 203
 1523 CGACGAT-----GGCGACTCGATGAAGATCCACCGATGAGGACTT 1564
 203 xLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIleGl 223
 1565 C---AAGCCCAACGAGACGAGTCCGATGTGCCCGGAGGAGTATGACAGCAACGCTGGAGAG 1621
 223 yThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlySe 243
 1622 TGATTCGGACGAT-----GACAGCGATGCTAGTGC-----GGCGG 1657
 243 rAsnAspIleMetGlySerThrAsnPhelysLeuLeuProGlyArgGluGlyAsnArgVa 263
 1658 AGCGGACAGCGCGCGCCCAAGAAAAGAGAGAGAGTCCGAGAGAAAAGAGAGAAA 1717
 263 lAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrProAlaApr 283
 1718 GGAGAAAACACACAGGAGAGAGAGAGAGAG-----AAACC 1756
 283 oSerLysGluLysArgLysGluGlySer----- 292
 1757 CTCCAAGAGAGAGAGGACTCTGGCAACCCCAAGCGCGCCACCGCTTTTCATGCTCTG 1816
 293 ----SerAspAlaAlaGluSer-----ThrAsnTyrAsnGluI 304
 1817 GCTGAACGACACCGCGGAGAGCATCAAGAGGAGAAATCCGGGCATAAAGTTTACCGAGAT 1876
 304 eProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnAsnGlnAl 324
 1877 CGCCAAAGAGCGCGCGAGATGTGGAAGAGAGCTGAAGGACAAAGTCCCAAGTGGAGGATGC 1936
 324 aThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGlyLeuProIlePr 344
 1937 GCGCGCCCAAGGACAGACGCGCTAC----- 1961
 344 oSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsnGlyProSerHi 364
 1961 ----- 1961
 364 sGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArgGlnAsnAsnSe 384
 1962 -----CACGACGAGATGCGCACTACAAAGCTGAAAGCGGCGGTGACAG 2005
 384 rThrArgAsnLysGlyMetProGlnGlyLysGlySerTyrGlyArg-----GlnProHi 402
 2006 CGACACGAGAGAGGT-----GMAAGTCTCCAAAGCGCGCAAGACGAGGCTTC 2056
 402 sSerAsnArgArg-----PheSerSerArgArg-----ArgAs 413
 2057 TCCATCCCAAGAGCGCAATACCTCGGCGAGCGGCTTCAAGAGCAAGAGTACATTTCCGA 2116
 413 pAspSerSerGluSerSerAspSerGlySerSerSerGlu----- 426
 2117 CGACGACTCCACAGCTCCGACCGAGGAGGACAGGACGCTGCCCAAGAGAGAGCA 2176
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RESULT 8

US-08-866-840-5

; Sequence 5, Application US/08866840

; Patent No. 6475791

; GENERAL INFORMATION:

; APPLICANT: Lippard, Stephen J.

; APPLICANT: Essigmann, John M.

; APPLICANT: Donahue, Brian A.

APPLICANT: Toney, Jeffrey H.
 APPLICANT: Bruhn, Suzanne L.
 APPLICANT: Pil, Pieter M.
 APPLICANT: Brown, Steven
 APPLICANT: Kellest, Patti
 TITLE OF INVENTION: Uses For DNA Structure-Specific
 TITLE OF INVENTION: Recognition Proteins
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Patent Administrator, Testa, Hurwitz & Thibault
 STREET: 53 State Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 FILING DATE: 02-JUN-1997
 APPLICATION NUMBER: US/08/866,840
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Fenton, Gillian M.
 REGISTRATION NUMBER: 36,508
 REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-248-7000
 TELEFAX: 617-248-7100
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2384 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Drosophila melanogaster
 IMMEDIATE SOURCE:
 CLONE: Drosophila SSRP - composite sequence
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT: 2
 MAP POSITION: 60A 1-4
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 123..2291
 US-08-866-840-5

Alignment Scores:
 Pred. No.: 0.000795 Length: 2384
 Score: 138.50 Matches: 99
 Percent Similarity: 31.91% Conservative: 50
 Best Local Similarity: 21.20% Mismatches: 136
 Query Match: 6.08% Indels: 182
 DB: 4 Gaps: 23

US-09-700-696C-2 (1-430) x US-08-866-840-5 (1-2384)

Qy 16 GlyLeuArgMetSerIleTyProLysSerThrGly-AsnLysGlyPheGluAspGlyAs 35

Db 1187 GGAGGAGGAGGATTCATATATATCCCAAGCCACCGTGCATATCCGGTTTGAGGAG- 1241

Qy 35 pAspAlaIleSerLysLeuHisAspGlnGluLutyrGlyAla- 49

Db 1242 -----ATTAGTTCGTGAACCTTGCCCGCAGCGCGGATCCACCGCATCTTTCGACTT 1294

Qy 50 ----AlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAlaIleLysLe 68

Db 1295 CGAAGTACGCTCAAGAACCGAAGTGTTCACATCTTCTCTCTCCATC----- 1340

Qy 68 uLeuGlyGluGluAsnLysGluAsnThrProArgAsnValLeuAsnIleIleProAlaSe 88

Db 1341 -----CAGAGGAGGAG----- 1352

Qy 88 rMetAsnTyAlaLysAlaHisSerLysAspLysLysLysProGlnArgAspSerGlnAl 108

Db 1353 -----TATGCCAAGCTC----- 1364

Qy 108 aGlnLysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyLe 128

Db 1365 -----TTCGACTACAT 1375

Qy 128 uLys-----HisLeuSerLysValLysLysIleProSerAspPheGluGlySe 144

Db 1376 CACACAGAGAAGTTGCATGTCAGCAACATGGCGAAG-----GACAAGAG 1420

Qy 144 rGlyTyThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGl 164

Db 1421 CGGCTACAGGACGCG-----GACTTTGGTGATTCGGAC-----AACGAGAA 1462

Qy 164 yGlnProPheLysAspIleProGly-----LysGlyGluAlaThrGlyProAspLeuGluGl 183

Db 1463 CGAACCCAGATGCTATCTGGCTCGCTCAAGCTGAGCGGAGGAAAGAGGAGGAGCA 1522

Qy 183 yLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspTh 203

Db 1523 CGACCAT-----GGCGACTCGGTGAGAGTCCAGGATCCAGGATGAGGACTT 1564

Qy 203 rLysLysProGlyTyAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIleGl 223

Db 1565 C---AAGCCCAACGAGAACGAGTCCGATGTGCCGAGGAGTATGACAGCAACGTCGAGAG 1621

Qy 223 yThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlySe 243

Db 1622 TGATTCGGACGAT-----GACAGCGATGCTAGTGGC-----GGCGG 1657

Qy 243 rAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsnArgVa 263

Db 1658 AGCGGACAGCGCGCGCCACAGAAAAGAGAGAGAAAGTCCGAGAGAGAGAGAGAAA 1717

Qy 263 lAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyProAlaPr 283

Db 1718 GGAGAAAAAACACAGGAGAGAGAGAGAGAGAG-----AAACC 1756

Qy 283 oSerLysGluLysArgLysGluGlySer----- 292

Db 1757 CTCGAGAGAGAGAGAGAGACTCTGGCAACCCAGCGCGCCACCACCGCTTTCATGCTCG 1816

Qy 293 -----SerAspAlaAlaGluSer-----ThrAsnTyAsnGluL 304

Db 1817 GCTGAACGACACGCGGAGAGCATCAAGAGGGGAAATCCGGGCATAAAGTTACCGAGAT 1876

Qy 304 eProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAl 324

Db 1877 CGCCAGAGAGCGCGCGAGATGTGGAGGAGCTGAAGGACCAAGTCCCAAGTGGGAGGATGC 1936

Qy 324 aThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGlyLeuProIlePr 344

Db 1937 GGCGGCCAACGACACAGCAGCGCTAC----- 1961

Qy 344 oSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsnGlyProSerHi 364

Db 1961 ----- 1961

Qy 364 sGluAsnIleIleThrHisGlyArgLysTyHisTyValProHisArgGlnAsnAsnSe 384

Db 1962 -----CACGACGAGATGCGCAACTACAGCTTGAAGCGGCGGTGACAG 2005

Qy 384 rThrArgAsnLysGlyMetProGlnGlyLysGlySerTyGlyArg-----GlnProHi 402

Db 2006 CGACAACGAGAGAGAGGT-----GGAAGTCTCCAAAGAGCGGAGCGGCTTC 2056

Qy 402 sSerAsnArgArg-----PheSerSerArgArg-----ArgAs 413

Db 2057 TCCATCCAGAGGCGAATACCTCGGCGAGCGGCTTCAAGACGAGGAGTACATTTCCGGA 2116
Qy 413 pAspSerSerGluSerSerAspSerGlySerSerSerGlu----- 426
Db 2117 CGAGACTCCACCGAGCTCCGAGGAGGAGGAGGACACAGCGCTGCCAAGAGAGAGCA 2176
Qy 427 -----SerAspGlyAsp 430
Db 2177 GCCCCATCCGACGCGGAT 2195

RESULT 9

PCT-US92-11107-10
Sequence 10, Application PC/TUS9211107
GENERAL INFORMATION:
APPLICANT: Donahue, Brian A.
APPLICANT: Toney, Jeffrey H.
APPLICANT: Bruhn, Suzanne L.
APPLICANT: Pil, Pieter M.
APPLICANT: Brown, Steven
APPLICANT: Kellest, Patti
APPLICANT: Essigmann, John M.
APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structure Specific Recognition
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11107
FILING DATE: 19921218

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/539,906
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4787AAA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-861-6240

TELEFAX: 617-861-9540

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 2384 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: Drosophila melanogaster

IMMEDIATE SOURCE:

CLONE: Drosophila SSRP - composite sequence

POSITION IN GENOME:

CHROMOSOME/SEGMENT: 2

MAP POSITION: 60A 1-4

FEATURE:

NAME/KEY: CDS

LOCATION: 123..2291

PCT-US92-11107-10

Alignment Scores: 0.000795 Length: 2384
Pred. No.: 138.50 Matches: 99
Score:

Percent Similarity: 31.91% Conservative: 50
Best Local Similarity: 21.20% Mismatches: 136
Query Match: 6.08% Indels: 182
DB: 5 Gaps: 23

US-09-700-696C-2 (1-430) x PCT-US92-11107-10 (1-2384)

Qy 16 GlyLeuArgMetSerIleTyProLysSerThrGly-AsnLysGlyPheGluAspGlyAs 35
Db 1187 GGAGCGAGGATTATCATCTATATCCACAGCCCGTCGCATATCCGCTTTTGAGGAG----- 1241
Qy 35 pAspAlaIleSerLysLeuHisAspGlnGluGluTyfGlyAla----- 49
Db 1242 -----ATTAGTTCTGGAACCTTTGCCGAGCGCGGATCCACGCGATCTTCGACTT 1294
Qy 50 -----AlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAlaIleLysLe 68
Db 1295 CGAAGTGACGCTCAAGAAGCGGAACCTGTTACATCTCTCTCCATC----- 1340
Qy 68 uLeuGlyGluGluAsnLysGluAsnThrProArgAsnValLeuAsnIleIleProAlaSe 88
Db 1341 -----GAGAAGGAGGAG----- 1352
Qy 88 rMetAsnTyfAlaLysAlaHisSerLysAspLysLysProGlnArgAspSerGlnAl 108
Db 1353 -----TATGCCAAGCTC----- 1364
Qy 108 aGlnLysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyfLe 128
Db 1365 -----TTGCACTACAT 1375
Qy 128 uLys-----HisLeuSerLysValLysLysIleProSerAspPheGluGlySe 144
Db 1376 CACACAGAGAAGTTGTCATGTCCAGCAACATGGCGAAG-----GACAAGAG 1420
Qy 144 rGlyTyfThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGl 164
Db 1421 CGGCTACAAGGAGCTG---GACTTTGGTGATTTCGGAC-----AACGAGAA 1462
Qy 164 yGlnProPheLysAspIleProGly---LysGlyGluAlaThrGlyProAspLeuGluGl 183
Db 1463 CGAACCCAGATGCTATCTGCTCGCTCAAGCTGAGCGGAGGAGGAGGAGGAGGAGCA 1522
Qy 183 yLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspTh 203
Db 1523 CGACGAT-----GGCGACTCGGATGAAGAGTCCACGAGTACGAGGACIT 1564
Qy 203 rLysLysProGlyTyfAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIleGl 223
Db 1565 C---AAGCCCAACGAGAACGAGTCCGATGTGCCGAGGAGTATGACAGCAACGTGGAGAG 1621
Qy 223 yThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlySe 243
Db 1622 TGATTCGACGAT-----GACAGCGATGCTAGTGGC-----GGCGG 1657
Qy 243 rAsnAspIleMetGlySerThrAsnPhelyGluLeuProGlyArgGluGluAsnArgVa 263
Db 1658 AGCGCACGACGCGCGCCCAAGAAAAGAGAGAGAGAGTCCGAGAGAGAGAGAGAGAAA 1717
Qy 263 lAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyfProProAlaPr 283
Db 1718 GGAGAAAAAACACAGAGAGAGAGAGACAAAG-----AAACC 1756
Qy 283 oSerLysGluLysArgLysGluGlySer----- 292
Db 1757 CTCCAAGAGAGAGAGAGACTCTCGCAAAACCAAGCGGCCACCACCGCTTTCATGCTCTG 1816
Qy 293 -----SerAspAlaAlaGluSer-----ThrAsnTyfAsnGluIl 304
Db 1817 GCTGACGACACGCGCGAGAGCATCAAGAGCGGAGAAAATCCGGGCATAAAGGTTACCGAGAT 1876
Qy 304 eProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAl 324
Db 324 -----

Db 1877 CGCCAAAGAGGGCGGAGATGCTGAAGAGGCTGAAGCAAGTCCAGTGGGAGATGC 1936
Qy 324 aThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGlyLeuProIlePr 344
Db 1937 GGCGCCCAAGGACAGCAGCGCTAC----- 1961
Qy 344 oSerArgGlyLeuAspAsnGluLysAsnGluMetAspSerPheAsnGlyProSerHi 364
Db 1961 ----- 1961
Qy 364 sGluAsnIleThrHisGlyArgLysTyrHisTyrValProHisArgGlnAsnAsnSe 384
Db 1962 -----CAGCAGGAGATCGGCACTACAGCCTCAAGCGGCGGTGACAG 2005
Qy 384 rThrArgAsnLysGlyMetProGlnGlyLysGlySerTyrGlyArg-----GlnProHi 402
Db 2006 CGACAAGAGAGGGT-----GGAAAGTCTCCAAAGAGCGCAAGCGGCGCTTC 2056
Qy 402 sSerAsnArg-----PheSerSerArgArg-----ArgAs 413
Db 2057 TCCATCCAAAGAGCGGAATACCTCGGCGAGCGGCTTCAAGAGCAAGAGTACATTTCGGA 2116
Qy 413 pAspSerSerGluSerAspSerGlySerSerSerGlu----- 426
Db 2117 CGAGACTCCACAGCTCCGACGACGAGAGGACACAGCGCTGCCAAGAGAGAGCAA 2176
Qy 427 -----SerAspGlyAsp 430
Db 2177 GCCCCCATCCGAGCGGAT 2195

RESULT 10
US-08-320-559-27
Sequence 27, Application US/08320559
Patent No. 5633135
GENERAL INFORMATION:
APPLICANT: Croce, Carlo
APPLICANT: Canaan, Eli
TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
TITLE OF INVENTION: Detection and Treatment of Acute Leukemias
TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
TITLE OF INVENTION: All-1 Region
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5633135ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,559
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/062,443
FILING DATE: 14 MAY 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/971,094
FILING DATE: 30-OCT-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,830
FILING DATE: 27-MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/805,093
FILING DATE: 11-DEC-91
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: TJU-0855
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 9370 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 469..4032
US-08-320-559-27

Alignment Scores:
Pred. No.: 0.0081 Length: 9370
Score: 137.00 Matches: 100
Percent Similarity: 34.70% Conservative: 61
Best Local Similarity: 21.55% Mismatches: 192
Query Match: 6.01% Indels: 113
Gaps: 17

US-09-700-696C-2 (1-430) x US-08-320-559-27 (1-9370)

Qy 37 AlaIleSerLysLeuHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnMet 56
Db 1938 GCAGCTGGACACTGGCTGACCAAAAGTCAGCCAGCAGCTGGCCACCAGAGGGCCCCAG 1997
Qy 57 GlnHisIleMetGlyProValThrAlaIleLysLeuGlyGluGluAsnLysGluAsn 76
Db 1998 GAGCAC---AGAGCCCCCAGCGCGCACCCAGAGTAGGAGGACGACGAGCGAGTGCAC 2054
Qy 77 ThrProArgAsnValLeuAsn-----IleIleProAlaSerMetAsnTyrAlaLysAla 94
Db 2055 GAGTC-AGGAGCATCTGATCCAAAGATCTCTCCC-----CTAAAGCT 2098
Qy 95 HisSerLysAspLysLysProGlnArg-----AspSerGlnAlaGln 109
Db 2099 CC-AGCAAGCCCCCGGCGCCACCCGAAAGCCCCCAGCGGAGAGGAGGTGTGAG 2157
Qy 110 LysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLeuLys 129
Db 2158 AGTCTCCGGCAGCAGGAGGCCCCCAAGAGCAACCGTTGGACCAACCAACCCAAA 2217
Qy 130 HisLeuSerLysValLysLysIleProSerAspPheGluGlySerGlyTyrThrAspLeu 149
Db 2218 -----AAACTGTCAAGGCTCTGCGCGGCGAGGTTCAAGGAGCGCTG 2262
Qy 150 GlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGlnProPheLysAsp 169
Db 2263 CAGGGGAAAGGAGGAGCGAGGCTTTCTTCTCTATGCTCCCGAGACGAGCTTCCAAAGAC 2322
Qy 170 IlePro-----GlyLysGlyGlu----- 175
Db 2323 AAGCCCCAAGTGAAGACGAAGAGAGCGGCCCCGGCGGCGAGCAAGCAAGCAAGCCAGCCA 2382
Qy 176 AlaThrGlyProAspLeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGlu 195
Db 2383 GCAGTCCCTCCCTGACTGAGAGCGAGCGGCCCCCAACCCAGTGGCGGCGGAGGAGCT 2442
Qy 196 AlaGluSer-----ThrHisLeuAspThrLysLysProGlyTyr----- 208
Db 2443 GCTCTCTCAGGCCCAAGAACCCCGGAAGGACAATGTTGGAGACAGACCCCTGAGCACTTT 2502
Qy 209 -----AsnGluIleProGluArgGluGluAsnGlyGlyAsnThr 221
Db 2503 GCTCTTGTTCCTGACTGAGAGCGAGCGGCCCCCAACCCAGTGGCGGCGGAGGAGCT 2562
Qy 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
Db 2563 AGTGGCTGCGGCCCAAGCCGCTGTGTGTCAGGAGGACAGCGCGGCAAGACAGACTCCCATTTG 2622


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Pred. No.: 0.00813 Length: 9391
Score: 137.00 Matches: 100
Percent Similarity: 34.70% Conservative: 61
Best Local Similarity: 21.55% Mismatches: 192
Query Match: 6.01% Indels: 113
DB: 1 Gaps: 17

US-09-700-696C-2 (1-430) x US-08-320-559-25 (1-9391)

QY 37 AlalieserLysLeuHisAspGlnGluGlyTyrGlyAlaAlaLeuLeuHisArgAsnMet 56
D 1959 GCAGCTGCACACCTGGCTGACCAAGTCAGCCAGCCAGCTGGCCAGCAGAGGCCCCCAG 2018
QY 57 GlnHisIleMetGlyProValThrAlaIleLysLeuLeuGlyGluGluAsnGlyAsn 76
D 2019 GAGCAC---AGAGCCCCCAGCGGCCACCCAGAGAGTAGGAGGAGCAGCAGCAGTGCAC 2075
QY 77 ThrProArgAsnValLeuAsn-----IleIleProAlaSerMetAsnTyrAlaLysAla 94
D 2076 GAGTC-AGGAGCATTCGATCCAAAGATCTCTCCC-----CTAAAGACT 2119
QY 95 HisSerLysAspLysLysProGlnArg-----AspSerGlnAlaGln 109
D 2120 CC-AGCAAGCCCCCGGCCGCCACCCGAAAGCCCCCACCACCCGGAAGAGAGAGTGTCCAG 2178
QY 110 LysSerProValLysSerLysThrHisArgIleGlnHisAsnIleAspTyrLeuLys 129
D 2179 AGTCTTCGGCACACAGAGAGCCCCCAAGAGGCAACCGTTGGACCAACACCCAAA 2238
QY 130 HisLeuSerLysValLysLysIleProSerAspPheGluGlySerGlyTyrThrAspLeu 149
D 2239 -----AAACCTGTCAAGGCTCTGCGCGGCGAGGTTTCAGGACAGCAGCTG 2283
QY 150 GlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGlnProPheLysAsp 169
D 2284 CAGGGGGAAGGAGCCAGGCTTCTTCCATAGCTCCCGAGCAGCAGCTTCCAAAGAC 2343
QY 170 IlePro-----GlyLysGlyGlu----- 175
D 2344 AAGCCCCAAGGTGAAGACGAAGAGCGGCCCGCGCGGCGAGCAAGCAACCAAGCCCA 2403
QY 176 AlaThrGlyProAspLeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGlu 195
D 2404 CAGTGTCCCCCTCCAGTGAGAGAGAGCAAGAGCTCCCTCCCTCCCTCTCTAG 2463
QY 196 AlaGluSer-----ThrHisLeuAspThrLysLysProGlyTyr--- 208
D 2464 GCTCTCTCAGGCCAGACCCCGGAGGACATGTGGAGGACAGGACCCCTGAGCAGCTT 2523
QY 209 -----AsnGluIleProGluArgGluGluAsnGlyLysThr 221
D 2524 GCTCTGTTCCTCAGTACAGGAGCCAGGCCCCACCCACAGTGGCGGCGGAGGAGCT 2583
QY 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
D 2584 AGTGGTGGCGGCAAGCCCTGTGTTCAGGAGGAGCAGCGGCAAGACAGACTCCCATTTG 2643
QY 242 GlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGlyAsn 261
D 2644 CCTTTGAGAGACACCAAGAGCTGCTCTCAGCGCTCAGGAGCAGCTCTCCCCCAAGAGCTTG 2703
QY 262 ArgVal-----AspAlaGlySerGlnAsnAla 270
D 2704 ATGGTGAAGATCACCTAGACTGCTCTCTCGATACCCAGCTCCCGGAGGAGGAGC 2763
QY 271 HisGlnGlyLysValGluPheHisTyrProProAlaProSerLysGluLysArgLysGlu 290
D 2764 CGCAGAGGAAGACAGCAATATAACAGCGGCCCGCAGGAGGAGGAGCAGACTCTCAGAG 2823
QY 291 GlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluIleProLysAsnGlyLysGly 310
D 2824 AGGAGCTCAGACAGCTCA-----AGCAAGTGTGCCAAAGAGAGAGGCT 2869

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311 SerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGlnLysGln 330
D 2869 GAAGCAGAAGAGAGACTGTGAT-----AACAGAAATC 2901
QY 331 ArgPheProSerLysGlyLysSerGlnGlyLeuProIleProSerArgGlyLeuAspAsn 350
D 2902 AGA-----CTGGAGAAG 2913
QY 351 GluIleLysAsnGluMetAspSerPheAsnGlyProSerHisGluAsnIleIleThr--- 369
D 2914 GAATCAATCAGACTCATCTTCATCTCCCAAGAAATCTTCTTAAACAAG 2973
QY 370 -----HisGlyArgLysTyrHisTyrValProHisArgGlnAsn 382
D 2974 CCTCCAGCCCTCTCAGCTCCCAAGAAAGAAATGCTCCCGCCGCCCTGCTCC 3033
QY 383 AsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySer----- 396
D 3034 TCTCTCTCCCAAGAGCAGCAGCCTGACCTTAAGAGGTCAAGCGGGAAGCAGACACC 3093
QY 397 TrpGlyArgGlnPro-----HisSerAsnArgPheSerSer 409
D 3094 TGTGGCAGAGACCTCCCAAGAGTCCAGCAGTACCAGAGCAACACAAAGACTTCTCC 3153
QY 410 ArgArgArgAspAspSerSerGluSerSerAspSerGlySerSerSerGlu----- 426
D 3154 ATTCCCAAGCAGAGAGAGTAGAGGGAAGGCTCCAGAAAGCTCTCTCGGAGCAGCAAGGCT 3213
QY 427 SerAspGlyAsp 430
D 3214 TCTTCGGAGAT 3225

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```

RESULT 14
US-08-545-860D-25
: Sequence 25, Application US/08545860D
: Patent No. 6040140
: GENERAL INFORMATION:
: APPLICANT: Croce, Carlo
: APPLICANT: Canaan, Eli
: TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
: TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
: TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
: NUMBER OF SEQUENCES: 94
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
: ADDRESSEE: No. 6040140ris
: STREET: One Liberty Place, 46th floor
: CITY: Philadelphia
: STATE: Pennsylvania
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM: disk
: MEDIUM TYPE: Floppy
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/545,860D
: FILING DATE: 07-MAR-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/04496
: FILING DATE: 22-APR-1994
: APPLICATION NUMBER: PCT/US92/10930
: FILING DATE: 09-DEC-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/327,392
: FILING DATE: 19-OCT-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/320,559
: FILING DATE: 11-OCT-1994
: PRIOR APPLICATION DATA:

```


CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
 ADDRESSEE: Norris
 STREET: One Liberty Place, 46th floor
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/04496
 FILING DATE:

CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: DeLuca Esq., Mark
 REGISTRATION NUMBER: 33,229
 REFERENCE/DOCKET NUMBER: TJU-1242
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9391 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 421..4053
 PCT-US94-04496-25

Alignment Scores:
 Pred. No.: 0.00813 Length: 9391
 Score: 137.00 Matches: 100
 Percent Similarity: 34.70% Conservative: 61
 Best Local Similarity: 21.55% Mismatches: 192
 Query Match: 6.01% Indels: 113
 DB: 5 Gaps: 17

US-09-700-696C-2 (1-430) x PCT-US94-04496-25 (1-9391)

QY 37 AlaIleSerLysLeuHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnMet 56
 DB 1959 GCAGCTGGCAACTGCTGACCAAGTCAGCCAGCCAGCTGGCCACACAGAGGCCCCAG 2018
 QY 57 GlnHisIleMetGlyProValThrAlaIleLysLeuGlyGluGluAsnLysGluAsn 76
 DB 2019 GAGCAC---AGAGCCCCCAGCGGCCACCCAGAGAGTAGAGGCGCAGCGAGTGGCCAC 2075
 QY 77 ThrProArgAsnValLeuAsn-----IleIleProAlaSerMetAsnTyrAlaLysAla 94
 DB 2076 GAGTC-AGGAGCATTCGATCCAAAGATCCCTCCC-----CTAAAGACT 2119
 QY 95 HisSerLysAspLysLysLysProGlnArg-----AspSerGlnAlaGln 109
 DB 2120 CC-AGCAAAAGCCCCCGGCCACCCAGAGCCGCCAGAGGAGGAGGAGTGTCTAG 2178
 QY 110 LysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyrLeuLys 129
 DB 2179 AAGTCTCCGCGCAGAGGAGGCCCCCAAGGCAACCGTTGGAAACCAACCAACCCAA 2238
 QY 130 HisLeuSerLysValLysLysIleProSerAspPheGluGlySerGlyTyrThrAspLeu 149
 DB 2239 -----AAACCTGTCAAGGCGCTCTGCCCGGCGCAGGTTTCACGGACCGAGCTG 2283
 QY 150 GlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGlnProPheLysAsp 169
 DB 2284 CAGGGGAAAGGAGGCCAGGGCTTCTTCTTATGGCTCCGAGACCGAGACTTCCAAAGAC 2343

QY 170 IlePro-----GlyLysGlyGlu----- 175
 DB 2344 AAGCCCAAGGTGAAGACGAAAGAGCGGCCCGCGCGAGCAAGCAAGCAAGCAAGCAAGCA 2403
 QY 176 AlaThrGlyProAspLeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGlu 195
 DB 2404 GCAGTGGCCCCCTCCAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2463
 QY 196 AlaGluSer-----ThrHisLeuAspThrLysLysProGlyTyr--- 208
 DB 2464 GCTCTCTCAGGCCAGAACCCCGAGAGCAATATGGAGGAGCAGAGCCCTCAGCAGCTTT 2523
 QY 209 -----AsnGluIleProGluArgGluGluAsnGlyGlyAsnThr 221
 DB 2524 GCTCTTGTTCCTGACTGAGAGCCAGGGCCACCCACAGTCGAGCGGAGCAGGAGCT 2583
 QY 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuValGlu 241
 DB 2584 AGTGGCTGCCCAAGCCCGTGTGTCTCCAGAGGAGCAGCGGCAAGACAGACTCCCATTTG 2643
 QY 242 GlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGlyGluAsn 261
 DB 2644 CTTTCAGAGACACCAAGCTGCTCTCAGCGCTCAGGAGCACTCTCCGCCCAAGCTTG 2703
 QY 262 ArgVal-----AspAlaGlySerGlnAsnAla 270
 DB 2704 ATGCTGAAGATCACCTCAGACCTCTCTCTCGATACCCACGCTCCCGGAGGGGAGC 2763
 QY 271 HisGlnGlyValGluPheHisTyrProAlaProSerLysGlnLysArgLysGlu 290
 DB 2764 CGCCAGAGAAAGCAGAGATATAACAGCGCCCGCAGGAGGAGGAGGAGGAGGAGGAG 2823
 QY 291 GlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluIleProLysAsnGlyLysGly 310
 DB 2824 AGGAGCTCAGACAGCTCA-----AGCAAGTTGGCCAAAAAGAGAAAGGTT 2868
 QY 311 SerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGln 330
 DB 2869 GAAGCAGAAAGAGAGACTGTGAT-----AACAGAGAAATC 2901
 QY 331 ArgPheProSerLysGlyLysSerGlnGlyLeuProIleProSerArgGlyLeuAspAsn 350
 DB 2902 AGA-----CTGGAGAG 2913
 QY 351 GluIleLysAsnGluMetAspSerPheAsnGlyProSerHisGluAsnIleThr--- 369
 DB 2914 GAATCAATCAACAGTCATCTTCATCTCTCCCAAGAAATCTTCTAAACAAAG 2973
 QY 370 -----HisGlyArgLysTyrHisTyrValProHisArgGlnAsn 382
 DB 2974 CCTCCAGGCCCTCTCACAGTCTCTCAAGAGAGAAATGCTCCCGCCGACCCGCTGTC 3033
 QY 383 AsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySer----- 396
 DB 3034 TCGTCTCCAGAGCCAGCCAAAGCCTGCATTTAAGAGGTCAAGCGGAGGAGGAGGAGCACC 3093
 QY 397 TrpGlyArgGlnPro-----HisSerAsnArgArgPheSerSer 409
 DB 3094 TGTGGCCAGGACCTCCCAAAAGTGCAGCAGTACCAAGAGCAACCAAGAGACTCTTCC 3153
 QY 410 ArgArgArgAspAspSerSerGluSerSerAspSerGlySerSerSerSerGlu----- 426
 DB 3154 ATTCCAAGCAGAGAGAGAGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3213
 QY 427 SerAspGlyAsp 430
 DB 3214 TCTTCGGAGAT 3225

Search completed: March 29, 2004, 04:20:40
 Job time : 182 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 29, 2004, 01:33:17 ; Search time 451 Seconds

(without alignments)
3549.654 Million cell updates/sec

Title: US-09-700-696C-2

Perfect score: 2279

Sequence: 1 VNKEYSISNKTENHGLRMS.....RRDSSGSSGSSGSSGCD 430

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2458946 seqs, 1861504846 residues

Total number of hits satisfying chosen parameters: 4917892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Db=Published Applications NA -QWTF=Fastap -SUPFI=rnpb -MINMATCH=0.1
-LOPCH=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR_SCORE=ptc -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09700696@cgn_1_157@runat_24032004_151402_1162
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:
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5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:
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10: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:
14: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:
17: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:
18: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	2279	100.0	1655	12	US-10-438-181A-1	Sequence 1, Appli
2	2276	99.9	1575	14	US-10-311-840-2	Sequence 2, Appli
3	2276	99.9	1662	14	US-10-311-840-3	Sequence 3, Appli
4	2276	99.9	1876	10	US-09-794-422-33	Sequence 33, Appl
5	2276	99.9	1969	10	US-09-794-422-45	Sequence 45, Appl
6	2276	99.9	2013	12	US-10-438-181A-26	Sequence 26, Appl
7	2276	99.9	2019	10	US-09-794-422-5	Sequence 5, Appli
8	2276	99.9	2112	10	US-09-794-422-7	Sequence 7, Appli
9	993.5	43.2	1682	10	US-09-794-422-3	Sequence 3, Appli
10	938.5	41.2	1655	10	US-09-794-422-1	Sequence 1, Appli
11	149.5	6.6	1889	15	US-10-369-493-39715	Sequence 39715, A
12	148.5	6.5	8201	14	US-10-363-798-1	Sequence 1, Appli
13	148	6.5	3045	15	US-10-108-260A-1338	Sequence 1338, Ap
14	148	6.5	4985	12	US-10-210-172-65	Sequence 65, Appl
15	148	6.5	5721	9	US-09-785-770A-15	Sequence 15, Appl
16	148	6.5	5964	12	US-10-210-172-63	Sequence 63, Appl
17	148	6.5	8121	9	US-09-785-770A-14	Sequence 14, Appl
18	140	6.1	2673	14	US-10-153-668-301	Sequence 301, App
19	140	6.1	4839	14	US-10-101-510-396	Sequence 396, App
20	139	6.1	2381	15	US-10-104-047-1415	Sequence 1415, Ap
21	139	6.1	35465	14	US-10-161-572-6	Sequence 6, Appli
22	139	6.1	36991	14	US-10-161-572-8	Sequence 8, Appli
23	137	6.0	3668	15	US-10-108-260A-1304	Sequence 1304, Ap
24	137	6.0	9390	14	US-10-205-823-263	Sequence 263, App
25	135	5.9	5406	12	US-10-615-383-1	Sequence 1, Appli
26	134.5	5.9	3495	12	US-10-424-599-116489	Sequence 116489,
27	134.5	5.9	4084	13	US-10-153-273-1	Sequence 1, Appli
28	134	5.9	1446	14	US-10-156-761-4465	Sequence 4465, Ap
29	134	5.9	2254	14	US-10-198-846-13929	Sequence 13929, A
30	134	5.9	9025608	14	US-10-156-761-1	Sequence 1, Appli
31	133.5	5.9	1960	9	US-09-864-761-4620	Sequence 4620, Ap
32	133.5	5.9	7058	14	US-10-287-218-38	Sequence 38, Appl
33	133	5.8	3876	12	US-10-312-353-68	Sequence 68, Appl
34	132.5	5.8	2594	15	US-10-108-260A-355	Sequence 355, App
35	132	5.8	4899	12	US-10-282-122A-34253	Sequence 34253, A
36	131.5	5.8	2930	12	US-10-240-425-1324	Sequence 1324, Ap
37	131.5	5.8	4278	12	US-10-302-172-156	Sequence 156, App
38	131	5.7	2025	9	US-09-834-975-822	Sequence 822, App
39	130.5	5.7	1083	12	US-10-424-599-26623	Sequence 26623, A
40	130.5	5.7	1453	13	US-10-001-835-66	Sequence 66, Appl
41	130.5	5.7	1769	12	US-10-424-599-129848	Sequence 129848,
42	130.5	5.7	1923	12	US-10-282-122A-15136	Sequence 15136, A
43	130.5	5.7	2609	15	US-10-104-047-1365	Sequence 1365, Ap
44	130.5	5.7	3316	14	US-10-133-013-166	Sequence 166, App
45	130.5	5.7	5469	15	US-10-341-434-94	Sequence 94, Appl

ALIGNMENTS

RESULT 1

US-10-438-181A-1

; Sequence 1, Application US/10438181A

; Publication No. US20040053389A1

; GENERAL INFORMATION:

; APPLICANT: Rowe, Peter Stanley Nicola

; TITLE OF INVENTION: NO. US20040053389A1el Polypeptide Hormone-Phosphatonin

; FILE REFERENCE: BEAR-005CIP

; CURRENT APPLICATION NUMBER: US/10/438,181A

; CURRENT FILING DATE: 2003-05-13

; PRIOR FILING DATE: 2002-04-25

; PRIOR FILING DATE: 2002-04-25

; PRIOR FILING DATE: 1999-11-04

; PRIOR APPLICATION NUMBER: PCT/EP99/03403

; PRIOR FILING DATE: 1999-05-18

; PRIOR APPLICATION NUMBER: GB 9810681.8

; PRIOR FILING DATE: 1998-05-18

; PRIOR APPLICATION NUMBER: GB 9819387.3

; PRIOR FILING DATE: 1998-09-04

; NUMBER OF SEQ ID NOS: 55

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1655

TYPE: DNA
ORGANISM: Homo sapien
US-10-438-181A-1

Alignment Scores:
Pred. No.: 1,01e-214 Length: 1655
Score: 2279.00 Matches: 430
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-700-696C-2 (1-430) x US-10-438-181A-1 (1-1655)

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QY 1 ValAsnLysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSer 20
DB 1 GTGAATAAAGAAATATAGTATCATCAAAAGAGAAATCTCAAAATGGCCCTGAGGATGCA 60

QY 21 IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLys 40
DB 61 ATTATCTTARGTCACTGGGAATAAAGGTTTGAGGATGGAGATGATGCTATCAGCAA 120

QY 41 LeuHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnMetGlnHisIleMet 60
DB 121 CTACATGACCAAGAGATATGGCGCAGCTCTCATCAGAAATAACATGCAACATATAATG 180

QY 61 GlyProValThrAlaIleLysLeuLeuGlyGluAsnLysGluAsnThrProArgAsn 80
DB 181 GGCCCAAGTACTCGGATTAACCTCTGGGGGAGAGAAACAAAGAGAAACACACCTAGGAAT 240

QY 81 ValLeuAsnIleProLysSerMetAsnTyrAlaLysAlaHisSerLysAspLys 100
DB 241 GTTCTAAACATAATCCAGCAAGTATGAATTAATGCTAAAGCACACTCGAAGGATAAAAAG 300

QY 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
DB 301 AAGCCTCAAGAGATTCCTCAAGCCCAAGAAAGTCCAGTAAAGCAAAAGCAACCCATCT 360

QY 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAsp 140
DB 361 ATTCACACACAACTTACCTACCTAAACATCTCTCAAAAGTCAAAAAATCCCAAGTGAT 420

QY 141 PheGluGlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPhe 160
DB 421 TTTGAAGGCGCGGTATATACAGATCTTCAAGAGAGAGGGGACATGATATATCTCTTTC 480

QY 161 SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyAlaThrGlyProAsp 180
DB 481 AGTGGGACGCGCAACCTTTTAAAGACATCTCTGGTAAAGGAGAACTACTGGTCTGAC 540

QY 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
DB 541 CTAGAAGGCAAGATATTCACAGGGTTTTCAGGCGCCCAAGTGAAGCTGAGATCTCAT 600

QY 201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyLysAsn 220
DB 601 CTTGACACAAAAGCCAGGTTATATGATATCCAGAGAGAGAGAAATGGTGAAT 660

QY 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValSerLeuVal 240
DB 661 ACCATTGGAACCTAGGATGAAATCGCGAAAGAGCGAGATGCTGTTGATGTCAGCCTTGA 720

QY 241 GluGlySerAsnAspIleMetGlySerThrAsnPhelLysGluLeuProGlyArgGluGly 260
DB 721 GAGGCGAGCAACGATATCATGGGTAGTACCAATTTTAAAGGAGCTCCCTGGAGAGAGGA 780

QY 261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrPro 280
DB 781 AACAGAGTGGATGCTGCGAGCCAAAATGCTCAACAGGGAAGGTTGAGTTTCAATACCT 840

QY 281 ProLysSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn 300
DB 841 CCTGCACCTTCAAAAGAGAGAAAGAAAGAGGCGAGTGTGATGCGCTGAAGTACCAAC 900

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QY 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
DB 901 TATAATGAATTCCTAAAAATGCAAGGCACTACAGAAAGGGTGTGATCATTTCTAAT 960

QY 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
DB 961 AGGAACCAAGCAACCTTAATGAAACCAAGAGTTTCTTAGTAGGCGCAAAAGTCAGGCG 1020

QY 341 LeuProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsn 360
DB 1021 CTGCCCATTCCTTCTCGTGTCTTGATAATGAATCAAAACGAAATGATGATTCCTTTAAT 1080

QY 361 GlyProSerHisGluAsnIleThrHisGlyArgLysTyrHisTyrValProHisArg 380
DB 1081 GGCCCAAGTACTGAGATATATAACACATGCGAGAAATATCATTTATGACCCACAGA 1140

QY 381 GlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTrpGlyArgGln 400
DB 1141 CAAAATAAATTCACAGGAATAGGGTATGCCCAAGGGAAGGCTCCTGGGGTAGACAA 1200

QY 401 ProHisSerAsnArgPheSerSerArgArgAspAspSerSerGluSerSerAsp 420
DB 1201 CCCATTCCAACAGAGGTTTAGTTCCGTTAGAGGGATGACAGTAGTAGTCATCTGAC 1260

QY 421 SerGlySerSerGluSerAspGlyAsp 430
DB 1261 AGTGGCAGTTCAAGTGAGAGCGATGGTGAC 1290

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RESULT 2

US-10-311-840-2
Sequence 2, Application US/10311840
Publication No. US20030175808A1
GENERAL INFORMATION:
APPLICANT: KUOKAWA, Tomofumi
APPLICANT: YAMADA, Takao
APPLICANT: MORIMOTO, Shigeto
TITLE OF INVENTION: No. US20030175808A1: Protein and its DNA
FILE REFERENCE: 2738050P
CURRENT APPLICATION NUMBER: US/10/311,840
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: PCT/JP01/05263
PRIOR FILING DATE: 2001-06-20
PRIOR APPLICATION NUMBER: JP 2000-191088
PRIOR FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 2
LENGTH: 1575
TYPE: DNA
ORGANISM: Human
US-10-311-840-2

Alignment Scores:
Pred. No.: 1.87e-214 Length: 1575
Score: 2276.00 Matches: 429
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.77% Mismatches: 0
Query Match: 99.87% Indels: 0
DB: 14 Gaps: 0

US-09-700-696C-2 (1-430) x US-10-311-840-2 (1-1575)

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QY 1 ValAsnLysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSer 20
DB 286 CTGAATAAAGAAATATAGTATCATCAAAAGAGAAATCTCAAAATGGCCCTGAGGATGCA 345

QY 21 IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLys 40
DB 346 ATTTATCTTAACTCACTGGGAATAAAGGTTTGAGGATGGAGATGATGCTATCAGCAA 405

QY 41 LeuHisAspGlnGluGluTyrGlyAlaAlaLeuIleArgAsnMetGlnHisIleMet 60
DB 406 CTACATGACCAAGAGAGATATGGCGCAGCTCTCATCAGAAATAACATGCAACATATAATG 465

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QY 61 GlyProValThrAlaIleLysLeuLeuGlyGluGluAsnLysGluAsnThrProArgAsn 80
Db 466 GGGCCAGTGTGCTGATTAACCTCTCTGGGGAGAGAAACAAAGAGAACACACCTAGGAAT 525
QY 81 ValLeuAsnIleLeuProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
Db 526 GTTCTAAACATAATCCAGCAGTATGATTAATGCTAAAGCAGACACTCGAAGGATAAAAG 585
QY 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
Db 586 AAGCCTCAAGAGATTCCTCAAGCCAGAAAGTCCAGTAAAGCAAAAGCAACCCATCGT 645
QY 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAsp 140
Db 646 ATTCAACACACATTTAGCTACCTAAACATCTCTCAAAAGTCAAAAGCAAAATCCCAAGTAT 705
QY 141 PheGluGlySerGlyTyrThrAspLeuGlnArgGlyAspAsnAspIleSerProPhe 160
Db 706 TTTGAAGGAGCGGTTATACAGATCTTCAAGAGAGGGGACATGATATATCTCTCTTC 765
QY 161 SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp 180
Db 766 AGTGGGACGGCCAACTTTTAAAGCATTTCTGGTAAAGGAGAGCTACTGCTCTGAC 825
QY 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
Db 826 CTAGAAGGCAAGATATTCACACAGGTTTGCAGGCCCAAGTGAAGCTGAGAGTACTCAT 885
QY 201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyLysAsn 220
Db 886 CTTGACACAAAAGCCAGGTATATAGATGCCAGAGAGAGAAAGTGTGGAAT 945
QY 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuVal 240
Db 945 ACCATTGGAACCTAGGATGAAATCTCGAAGAGGAGAGATGCTGTGATGTCAGCCTTGA 1005
QY 241 GluGlySerAsnAspIleMetGlySerThrAsnAspLysGluLeuProGlyArgGluGly 260
Db 1006 GAGGCGAGCAACGATATATGCTGCTACCAATTTTAAAGGAGCTCCCTGGAAGAGAGA 1065
QY 261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrPro 280
Db 1066 AACAGAGTGTGCTCTGGCAGCCAAAATGCTCACCAGGGAAGGTTGAGTTTCAATACCT 1125
QY 281 ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn 300
Db 1126 CCTGCACCTTCAAAAGAGAAAGAAAGAGAGGAGGAGTGTGATGAGTCAAGAGTACCAAC 1185
QY 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
Db 1186 TATAATGAAATCTCTAAATGTCAAAGGCGAGTACCAGAAAGGGTGTAGATCATTTCTAAT 1245
QY 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
Db 1246 AGGAACCAAGCAACCTTAAATGAAACAAAGGTTTCTAGTAAAGGCAAAAGTCAAGGC 1305
QY 341 LeuProIleProSerArgLysLeuAspAsnGluIleLysAsnGluMetAspSerPheAsn 360
Db 1306 CTGCCATTCCTTCTGCTGCTTGATATGAAATCAAAACGAAATGGAATTCCTTTAAT 1365
QY 361 GlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArg 380
Db 1366 GGCCCCAGTCATGAGATATAAATACACATGGCAGAAATATCATTTATGTTACCCCAAGA 1425
QY 381 GlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTyrArgGln 400
Db 1426 CAATATATCTACACGGATAGGGTATGCCACAGGGAAGGCTCTCTGGGTAGACAA 1485
QY 401 ProHisSerAsnArgArgPheSerSerArgArgArgAspAspSerSerGluSerSerAsp 420
Db 1486 CCCCATTCACAGAGGTTTAGTTCCTCCGTAGAGGGATGACAGTAGTAGTCTATCTGAC 1545

QY 421 SerGlySerSerSerGluSerAspGlyAsp 430
Db 1546 AGTGGCAGTTCAAGTGAGAGCGATGCTGAC 1575
RESULT 3
US-10-311-840-3
; Sequence 3, Application US/10311840
; Publication No. US20030175808A1
; GENERAL INFORMATION:
; APPLICANT: KUROKAWA, Tomofumi
; APPLICANT: YAMADA, Takao
; APPLICANT: MORIMOTO, Shigeto
; TITLE OF INVENTION: No. US20030175808A1el Protein and its DNA
; FILE REFERENCE: 2738USOP
; CURRENT APPLICATION NUMBER: US/10/311,840
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: PCT/JP01/05263
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: JP 2000-191088
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 3
; LENGTH: 1662
; TYPE: DNA
; ORGANISM: Human
US-10-311-840-3
Alignment Scores:
Pred. No.: 2,01e-214 Length: 1662
Score: 2276.00 Matches: 429
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.77% Mismatches: 0
Query Match: 99.87% Indels: 0
Gaps: 0
DB: 14
US-09-700-696C-2 (1-430) x US-10-311-840-3 (1-1662)

QY 1 ValAsnLysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSer 20
Db 293 CTGAATTAAGAATATAGTATATCAGTAACAAAGAGAAATACTCACAAATGGCCCTGAGATGTCA 352
QY 21 IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLys 40
Db 353 ATTTATCTTAAGTCACTGGGAATTAAGGGTTTGAGGATGGAGATGATGTCATCAGCAA 412
QY 41 LeuHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMet 60
Db 413 CTACATGACCAAGAAGAAATATGGCCAGCTCTCATCAGAAATAACATGCAACATATAATG 472
QY 61 GlyProValThrAlaIleLysLeuLeuGlyGluAsnLysGluAsnThrProArgAsn 80
Db 473 GGGCCAGTGTGCTGCAATTAACCTCTGGGGAGAGAAACAAAGAGAACACACCTAGGAAT 532
QY 81 ValLeuAsnIleIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
Db 533 GTTCTAAACATAATCCAGCAGTATGATTAATGCTAAAGCAGACACTCGAAGGATAAAAG 592
QY 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
Db 593 AAGCCTCAAGAGATTCCTCAAGCCAGAAAGTCCAGTAAAGCAAAAGCAACCCATCGT 652
QY 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAsp 140
Db 653 ATTCACACACACATGACTACTTAAACATCTCTCAAAAGTCAAAAGATCCCCAGTGTAT 712
QY 141 PheGluGlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPhe 160
Db 713 TTTGAAGCAGCGGTATACAGATCTTCAAGAGAGAGGGGACATGATATATCTCTCTTC 772
QY 161 SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp 180
Db 773 AGTGGGAGCGGCCAACCTTTTAAAGACATTTCTGTTAAGGAGAGAGCTACTGCTCTGAC 832

181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
Db 833 CTAGAAGGCAAGATATTCAACAGGGTTTGACGGCCCAAGTGAAGCTGAGACTCAT 892

201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyLys 220
Db 893 CTGACACAAAAAAGCCAGTTATATGAGATCCACAGAGAGAGAAATGGTGGAAAT 952

221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuVal 240
Db 953 ACCATTGGAACTAGGATGAACTGCGAAAGAGGAGATGCTGTTGATGTGACGCTTGA 1012

241 GluGlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGly 260
Db 1013 GAGGGCAGCAACGATATCATGGTGTAGTACCAATTTTAAGGAGCTCCCTGGAGAGAGGA 1072

261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyValGluPheHisTyrPro 280
Db 1073 AACAGAGTGGATGCTGGCAGCCAAATGCTCCACAGGAGGAGGTGTAGTTCAATACCT 1132

281 ProAlaProSerLysLysLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn 300
Db 1133 CTGCAACCTTCAAAAGAGAAAAAGAAAGAGGAGGAGTGTAGTGCAGCTGAAAGTACCAAC 1192

301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
Db 1193 TATATGAAATTCCTTAAATATGCAAGAGGAGGAGTACCAAGAGGAGGTGTAGTTCAAT 1252

321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
Db 1253 AGGAACCAAGCAACCTTAAATGAAAAAACAAGGTTTCTAGTAAAGGCAAAAAGTCAGGCG 1312

341 LeuProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsn 360
Db 1313 CTGCCATTCCTTCTCGTGCTTTGATATGAAATCAAAACGAAATGATTCCTTTAT 1372

361 GlyProSerHisGluAsnIleThrHisGlyArgLysTyrHisTyrValProHisArg 380
Db 1373 GGCCCCAGTCATGAGAAATATAAACAACATGGCAGAAATATCATTTATGATACCCACAGA 1432

381 GlnAsnSerThrArgAsnLysGlyMetProGlnGlySerThrGlyArgGln 400
Db 1433 CAATAATTTCTACAGGAATAGGGTATGCCAAGGAGAAAGGCTCCTGGGGTAGACAA 1492

401 ProHisSerAsnArgArgPheSerSerArgArgAspAspSerSerGluSerSerAsp 420
Db 1493 CCCATTCCACAGGAGTTTGTTCCTCGTAGAAGGGATGACAGTAGTGTGATCATCTGAC 1552

421 SerGlySerSerSerGluSerAspGlyAsp 430
Db 1553 AGTGGCAGTTCAAGTGAGCGGATGGTGAC 1582

RESULT 4

US-09-794-422-33
; Sequence 33 Application US/09794422
; Publication No. US2003016239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 1876

Alignment Scores: 2.35e-214 Length: 1876
Score: 2276.00 Matches: 429
Percent Similarity: 100.00% Conservatives: 1
Best Local Similarity: 99.77% Mismatches: 0
Query Match: 99.87% Indels: 0
DB: 10 Gaps: 0

US-09-700-696C-2 (1-430) x US-09-794-422-33 (1-1876)

Qy 1 ValAsnLysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSer 20
Db 238 CTGAATAAAGATATAGTATCAGTAAACAAGAGATACTCACAATGCCTCGAGGATGTCA 297

Qy 21 IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLys 40
Db 298 ATTATCTCTAAGTCAACTGGGAATAAAGGGTTTGAGGATGGAGATGATGCTATCAGCAA 357

Qy 41 LeuHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMet 60
Db 358 CTACATGACCAAGAAGAAATATGGCGAGCTCTCATCAGAAATTAACATGCAACATATAATG 417

Qy 61 GlyProValThrAlaIleLysLeuLeuGlyGluGluAsnLysGluAsnThrProArgAsn 80
Db 418 GGGCCAGTGTGGATTAACCTCTGGGGGAGAGAAACAAGAGAACACACCTAGGAAT 477

Qy 81 ValLeuAsnIleIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
Db 478 GTTCTAAACATAATCCCGCAAGATATGAAATATATGCTAAAGCACACTCGAAGAGATAAAAG 537

Qy 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
Db 538 AAGCCTCAAGAGATTCACAGATCTTCAAGAGAGAGGGGACAAATGATATATCTCTTTC 597

Qy 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysValLysIleProSerAsp 140
Db 598 ATTCAACACACAACTTGACTACCTTAAACATCTCTCAAAAGCTCAAAAAATCCCGAGTAT 657

Qy 141 PheGluGlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPhe 160
Db 658 TTTGAAGCGACGGTTTATACAGATCTTCAAGAGAGAGGGGACAAATGATATATCTCTTTC 717

Qy 161 SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp 180
Db 718 AGTGGGAGCGCCAACTTTTAAGGACATTCCTGTGTAAGAGAGAGGCTACTGTGCTGTAC 777

Qy 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
Db 778 CTAGAAGGCAAGATATATCAACAGGGTTTGCAGGCCCAAGTGAAGCTGAGAGTACTCAT 837

Qy 201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyLysAsn 220
Db 838 CTTGACACAAAAAGCCAGGTTATATGAGATCCACAGAGAGAGAGAAATGGTGGAAAT 897

Qy 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuVal 240
Db 898 ACCATTGGAACTAGGATGAACTGCGAAAGAGGAGCAGATGCTGTTGATGTGACGCTTGA 957

Qy 241 GluGlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGly 260
Db 958 GAGGCGACAGACGATATCATGGTGTAGTACCAATTTTAAGGAGCTCCCTGGAGAGAGGA 1017

Qy 261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyValGluPheHisTyrPro 280
Db 1018 AACAGAGTGGATGCTGGCAGCCAAATGCTCACAAGGAGGAGGTGTAGTTCAATACCT 1077

Qy 281 ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn 300
Db 1078 CTGCACCTTCAAGAGAGAAAAAGAAAGAGGAGGAGTGTGATGTCAGCTGAAAGTACCAAC 1137

QY 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
 Db 1138 TATAATGAATTCCTAAATAATGCGAAGCAGTACCAGAAAGGGGTAGATCAATCTTAAT 1197
 QY 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
 Db 1198 AGGAACCAAGCAACCTTAATGAAAACAAGAAGTTCTCTAGTAGGGCAAGTCAAGGC 1257
 QY 341 LeuProIleProSerArgGlyLeuAspAsnGluLysAsnGluMetAspSerPheAsn 360
 Db 1258 CTGCCCATTCCTCTCGTGTCTTGATAATGAATCAAAACGAAATGGATTCCTTTAAT 1317
 QY 361 GlyProSerHisGluAsnIleThrHisGlyArgLysTyrHisTyrValProHisArg 380
 Db 1318 GGCCCCAGTCATGAGATATATACACATGCGAGAAATATCATATGTACCCACAGA 1377
 QY 381 GlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTyrGlyArgGln 400
 Db 1378 CAAATAAATCTACACGAATAAGGGTATGCCACAAGGGAAAGGCTCTGGGGTAGACAA 1437
 QY 401 ProHisSerAsnArgArgPheSerSerArgArgAspAspSerSerGluSerSerAsp 420
 Db 1438 CCCATCCAAACAGGAGGTTTGTCTCCGTAGAAGGGATGACAGTAGTGAGTCATCTGAC 1497
 QY 421 SerGlySerSerSerGluSerAspGlyAsp 430
 Db 1498 AGTGGCAGTTCAAGTGAGAGCGATGGTGAC 1527
 RESULT 5
 US-09-794-422-45
 ; Sequence 45, Application US/09794422
 ; Publication No. US20030166239A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Brown, Thomas A.
 ; APPLICANT: De Wet, Jeffrey R.
 ; APPLICANT: Gowen, Lori C.
 ; APPLICANT: Hames, Lynn M.
 ; TITLE OF INVENTION: Mammalian Osteoregulins
 ; FILE REFERENCE: PCL0445
 ; CURRENT APPLICATION NUMBER: US/09/794,422
 ; CURRENT FILING DATE: 2001-02-27
 ; PRIOR APPLICATION NUMBER: 60/185,617
 ; PRIOR FILING DATE: 2000-02-29
 ; PRIOR APPLICATION NUMBER: 60/234,500
 ; PRIOR FILING DATE: 2000-09-22
 ; NUMBER OF SEQ ID NOS: 46
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 45
 ; LENGTH: 1969
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-794-422-45
 Alignment Scores:
 Pred. No.: 2,51e-214 Length: 1969
 Score: 2276.00 Matches: 429
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 99.77% Mismatches: 0
 Query Match: 99.87% Indels: 0
 DB: 10 Gaps: 0
 US-09-700-696c-2 (1-430) x US-09-794-422-45 (1-1969)
 QY 1 ValAsnLysGluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSer 20
 Db 331 CTGATTAAGAAATATAGTATCAGTAACAAGAAAGAACTCACAAATGGCTTGAGATGTC 390
 QY 21 IleTyrProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLys 40
 Db 391 ATTATCTTAAGTCAACTGGATTAAGGGTTTGGAGTGGAGATGATGATCATACAGAAA 450
 QY 41 LeuHisAspGlnGluTyrGlyAlaAlaLeuLysArgAsnAsnMetGlnHisIleMet 60

Db 451 CTACATGACCAAGAGAAATATGCGGAGCTCTCATCAGAATTAACATGCAACATATAATG 510
 QY 61 GlyProValThrAlaIleLysLeuLeuGlyGluAsnLysGluAsnThrProArgAsn 80
 Db 511 GGGCCAGTACTCGATTAACTCTCGGGGAAGAAAACAAGAGAACACACCTAGCAAT 570
 QY 81 ValLeuAsnIleIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
 Db 571 GTTCTAAACATATCCAGCAAGTATGAAATATGCTTAAGCACATCTCGAAGGATATAAAG 630
 QY 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
 Db 631 AAGCCTCAAAAGAGATTCCTCAAGCCCAAGAAAGTCCAGTAAAAAGCAAAAGACCCATCGT 690
 QY 121 IleGlnHisSerIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAsp 140
 Db 691 ATTCACACAACTATGACTACCTAAACATCTCTCAAAAGTCAAAATAATCCCCAGTGAT 750
 QY 141 PheGluGlySerGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPhe 160
 Db 751 TTTCAGGCGAGCGTTTATACAGATCTTCAAGAGAGAGGGGACAATGATATATCTCCTTTC 810
 QY 161 SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp 180
 Db 811 AGTGGGACCGCCCAACCTTTTAAGGACATCTCTGTAAGAGAGAGAGCTACTGTCTCTGAC 870
 QY 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
 Db 871 CTAGAAGGCAAGATATTTCAACAGGGTTTGCAGGCCCAAGTGAAGCTGAGAGTACTCAT 930
 QY 201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsn 220
 Db 931 CTTGACACAAAAGAGCCAGTTTATATGAGATCCAGAGAGAGAGAGAAATGGTGGAAAT 990
 QY 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuVal 240
 Db 991 ACCATTGGAAGTGGATGAACTGCGAAGAGAGCGAGATCTCTTGTATGTACGCTTGT 1050
 QY 241 GluGlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGly 260
 Db 1051 GAGGCGACCAACGATATCATGGGTAGTACCAATTTTAAAGAGAGCTCTCTGGAAGAGAGGA 1110
 QY 261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisTyrPro 280
 Db 1111 AACAGTGGATGCTGCGACCCAAATGCTCACCAAGGAGAGGTTGAGTTTCTATTACCT 1170
 QY 281 ProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsn 300
 Db 1171 CCTGCACCTCAAAAGAGAGAAAGAAAGAGAGGAGTGTGATGAGTGAAGTACCAAC 1230
 QY 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
 Db 1231 TATAATGAATTCCTCAAAATGGCAAGGAGTACCAGAAAGGTTGATGATCATTTCTAAT 1290
 QY 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
 Db 1291 AGGAACCAAGCAACCTTTAAATGAAAACAAGGTTTCTTAGTAAGGGCAAAAGTCAAGGC 1350
 QY 341 LeuProIleProSerArgGlyLeuAspAsnGluLysAsnGluMetAspSerPheAsn 360
 Db 1351 CTGCCCATTCCTCTCGTGTCTTGATAATGAATCAAAACGAAATGGATTCCTTTAAT 1410
 QY 361 GlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArg 380
 Db 1411 GGCCCCAGTCATGAGATATAATAACATGCGAAGAAATATCATATTATGATACCCACAGA 1470
 QY 381 GlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTyrGlyArgGln 400
 Db 1471 CAAATAAATCTACACGAATAAGGGTATGCCACAAGGAAAGGCTCTCTGGGGTAGACAA 1530
 QY 401 ProHisSerAsnArgArgPheSerSerArgArgAspAspSerSerGluSerSerAsp 420

474 CTGAATAAAGAAATATAGTATCAGTAACAAGAGAAATCTACAAATGCGCTGAGGATGCA 533
QY 21 IletyProLysSerThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLys 40
Db 534 ATTTATCTTAAGTCAACTGGGAATAAAGGGTTTGAGGATGGAGATGATGCTATCAGCAAA 593
QY 41 LeuHisAspGlnGluGlyThrGlyAlaAlaLeuIleArgAsnMetGlnHisIleMet 60
Db 594 CTACATGACCAAGAGAAATATGGCGCAGCTCTCATCAGAAATAACATGCAACATATATG 653
QY 61 GlyProValThrAlaIleLysLeuLeuGlyGluGluAsnLysGluAsnThrProArgAsn 80
Db 654 GGGCAGTGAAGTCTCGATTAAGTCTCGGGGAAGAAACAAAGAGAGACACACCTAGGAAT 713
QY 81 ValLeuAsnIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLys 100
Db 714 GTTCTAAACATAATCCAGCAGTATGATTAAGTAAAGCACACTCGAAGATAAAG 773
QY 101 LysProGlnArgAspSerGlnAlaGlnLysSerProValLysSerLysSerThrHisArg 120
Db 774 AAGCTCTCAAGAGATCCAGCCAGAAAGTCCAGTAAAGCAAAAGCAACCATCGT 833
QY 121 IleGlnHisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAsp 140
Db 834 ATTCAACACAACTTGAATCTCTCAAAAGTCAAAAGTCAAAAGTCAAAAGTCAAAAGTCA 893
QY 141 PheGluGlySerGlyThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPhe 160
Db 894 TTGGAAGCAGCGGTATACAGTCTTCAAGAGAGAGGGGCAATGATATATCTCTTC 953
QY 161 SerGlyAspGlyGlnProPheLysAspIleProGlyLysGlyGluAlaThrGlyProAsp 180
Db 954 AGTGGGACGGCAACCTTTTAAAGACATTTCTGTAAAGGAGAGAGTACTGGTCTGTAC 1013
QY 181 LeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHis 200
Db 1014 CTGAAAGGCAAGATATTCAACAGGTTTGAGGCGCCAGTGAAGCTGAGAGTACTCAT 1073
QY 201 LeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsn 220
Db 1074 CTTGACACAAAAAGCGGTATATAGATATAGATCCAGAGAGAGAGAAATGGTGAAT 1133
QY 221 ThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLeuVal 240
Db 1134 ACCATTGGAACTAGGATGAACTGCGAAAGAGGAGAGTCTGTGTATGATGACCTTTGA 1193
QY 241 GluGlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArgGluGly 260
Db 1194 GAGGCGAGCAACGATATATGCTAGTATGATCAATTTTAAAGAGTCTCTGCAAGAGAGGA 1253
QY 261 AsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyValGluPheHisTyrPro 280
Db 1254 AACAGAGTGATCTGGCAGCCAAATGCTCAAGAGGAGGAGTATGATGATGATGATGATG 1313
QY 281 ProAlaProSerLysGluLysArgLysGluGlySerAspAlaAlaGluSerThrAsn 300
Db 1314 CTGTCACCTTCAAAAGAGAAAGAAAGAGAGGAGGAGTATGATGATGATGATGATGATG 1373
QY 301 TyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsn 320
Db 1374 TATAATGAAATCTCTTAAATGCAAGAGGAGGAGTATGATGATGATGATGATGATGATG 1433
QY 321 ArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGly 340
Db 1434 AGNACCAAGCAACCTTAAATGAAACAAAGAGGTTCTCTAGTAAAGGCAAAAGTCAAGGC 1493
QY 341 LeuProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsn 360
Db 1494 CTGCCATCTCTCTGCTGCTTGTATGATGATGATGATGATGATGATGATGATGATGATG 1553
QY 361 GlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHisTyrValProHisArg 380
Db 1554 GGCCCCAGTCTATGAGATATATATACATGAGGAGAGAAATATCATTTATGATGATGATG 1613

QY 381 GlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTyrGlyArgGln 400
Db 1614 CAAATAATATTCACACGGAATAGGTATGCCACAGGGAAGAGCTCTCTGGGTAGACAA 1673
QY 401 ProHisSerAsnArgArgPheSerSerArgArgAspAspSerSerGlySerSerAsp 420
Db 1674 CCCCATTCCACAGGAGGTTTGTTCCTCCTAGAGGATGACAGTAGTGTGATCTCTGAC 1733
QY 421 SerGlySerSerSerGluSerAspGlyAsp 430
Db 1734 AGTGGCAGTTCAGTGAGAGCGATGGTGAC 1763

RESULT 9

US-09-794-422-3
; Sequence 3, Application US/09794422
; Publication No. US20030166239A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins
; FILE REFERENCE: PCI0445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1682
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-794-422-3

Alignment Scores:
Pred. No.: 3,96e-87 Length: 1682
Score: 983.50 Matches: 217
Percent Similarity: 62.56% Conservative: 52
Best Local Similarity: 50.47% Mismatches: 134
Query Match: 43.15% Indels: 27
DB: 10 Gaps: 8

US-09-700-696C-2 (1-430) x US-09-794-422-3 (1-1682)

QY 6 SerIleSerAsnLysGluAsnThrHisAsnGlyLeuArgMetSerIleTyrProLysSer 25
Db 166 AGCTGGCGCAATCAAGACAGCAATTCACAGGACTTGGCAGCATCTGTGTATCTGTATCCC 225
QY 26 ThrGlyAsnLysGlyPheGluAspGlyAspAlaIleSerLysLeuHisAspGlnGlu 45
Db 226 ACCTGTGATGAGCAGAGGATGGCAGAGTGTCTCTCTCCACCGCTGCCAGGAC 285
QY 46 GluTyrGlyAlaAlaLeuIleArgAsnMetGlnHisIleMetGlyProValThrAla 65
Db 286 AGGTATGGTGTGCTCTCTCTCAGAAATATCAGCAGCCTGTAAAGACTCTAGTACTGGG 345
QY 66 IleLysLeuLeuGlyGluGluAsnLysGluAsnThrProArgAsnValLeuAsnIle 85
Db 346 GCCAATCTAGGAGGAGGAAACACAGAGAGCTCAGAGTGTCTTAGCGTATTT 405
QY 86 ProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLysProGlnArgAsp 105
Db 406 CCAGCAGATGTCATGATGCTAAAGTCTCTTAAAGACATAAAGATCAAGAGATTAT 465
QY 106 SerGlnAlaGlnLysSerProValLysSer-----LysSerThrHisArgIleGln 122
Db 466 CTGTAAACCCAGAGACCGCGTCAAAAGCAACACACCAACACACCCGCCAGCCGA 525
QY 123 HisAsnIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAspPheGlu 142

Db 526 CGGACCACTCACTACCTGACACATCTCCACAGATCAAGAGACTCCCGAGTGGCTTGA 585
Qy 143 GlySerGlyThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGly 162
Db 586 GCGAGTGGCTCCCGAGATCTTCTAGTGGGGAGATAATGATGTCCTCCCTTTTCAGTGA 645
Qy 163 AspGlyGlnProPheLysAspIleProGlyLysGlyGluAla---ThrGlyProAspLeu 181
Db 646 GATGGGCAACATTTATGCACATCTCTGGCAAGGAGGTGCTGGGTCTGTCCTGAA--- 702
Qy 182 GluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeu 201
Db 703 -----AGCTCAACTAGTGGCCCCCTCTCAGGCTCCAGCAAGCTGAAAGTTATTGACCCA 756
Qy 202 AspThrLysLysProGlyTyraAsnGluProGluArgGluGluAsnGlyGlyAsnThr 221
Db 757 CATATGAGTGGACTAGGCTCTATGAGATCCCGGGAGAGAGACATGCTGGCAGTGC 816
Qy 222 IleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValSerLeuValGlu 241
Db 817 TATGCAACAGACAGACAAAGCTGCACAGGGGGGAGGCTCTGCAGAGTGGGAGGCTTGTGGGG 876
Qy 242 GlySerAsnAspIleMetGlySerThrAsnGlyLysGluLeuProGlyArgGluGlyAsn 261
Db 877 GCGAGCATGAATCAGAGGAGCACCATTTCAGGGAATCTCCCGGAAAGAGAGAAAC 936
Qy 262 ArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGluPheHisProPro 281
Db 937 AGAATTAATGCCCGGAGCCAAATGCTCATCAAGGAAAGTAGAATTTCACTATCCCAA 996
Qy 282 AlaProSerLysGluLysArgLysGluGlySerSerAspAlaAlaGluSerThrAsnTy 301
Db 997 GTGGCTTCAGAGAAAGTAAGGGGGCGTGGAGCATGCGAGGAGAGCT---GGTTAC 1053
Qy 302 AsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyValAspHisSerAsnArg 321
Db 1054 AACGAAATCCCAAGAGCAGCAAGTAGCTCTAGCAAGATGTCAGAGAGTCCCAAGGG 1113
Qy 322 AsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGlyLeu 341
Db 1114 AACCAATTAACTTGAATGTCAGAGCCAAAGATTTCAGGTAAAGGCAAGGAGGCGCCT 1173
Qy 342 ProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSerPheAsnGly 361
Db 1174 GCTGCTCCCTCTCACAGTCTTAGTAATGAGGTTAAAGTGAA----- 1215
Qy 362 ProSerHisGluAsnIleThrHisGlyArgLysTyHisTyValProHisArgGln 381
Db 1216 -----GAAAC-----CAATATGTTGTTCCATGCAAA 1242
Qy 382 AsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySerTrp---GlyArgGln 400
Db 1243 AATATCTTACCGGATTAAGGATGTCACGGGAGAGGCTCTGCGCTTCGAGAAGA 1302
Qy 401 ProHisSerAsnArgArgPheSerSerArgArgAspAspSerGluSerSerAsp 420
Db 1303 CCAATATCCACAGGCGCTAGCACCCGCCAAGA---GACAGAGAGAGTGGTCACTCC 1359
Qy 421 SerGlySerSerSerGluSerAspGlyAsp 430
Db 1360 AGTGGAGTTCTAGTGAGAGTCAATGTTGAC 1389

RESULT 10

US-09-794-422-1
; Sequence 1, Application US/09794422
; Publication NO. US2003016223A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Thomas A.
; APPLICANT: De Wet, Jeffrey R.
; APPLICANT: Gowen, Lori C.
; APPLICANT: Hames, Lynn M.
; TITLE OF INVENTION: Mammalian Osteoregulins

FILE REFERENCE: PC10445
; CURRENT APPLICATION NUMBER: US/09/794,422
; CURRENT FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,617
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/234,500
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1655
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-794-422-1

Alignment Scores:
Pred. No.: 1,05e-82 Length: 1655
Score: 938.50 Matches: 211
Percent Similarity: 59.95% Conservatives: 45
Best Local Similarity: 49.41% Mismatches: 146
Query Match: 41.18% Indels: 25
DB: Gaps: 8

US-09-700-696C-2 (1-430) x US-09-794-422-1 (1-1655)

Qy 9 AsnLysGluAsnThrHisAsnGlyLeuArgMetSerIleTyProLysSerThrGlyAsn 28
Db 146 AACCAAGGCAACATCCAC-----TTAGCATCTGTGAAGCTGAGCCCATGTTGGGT 196
Qy 29 LysGlyPheGluAspGlyAspAspAlaIleSerLysLeuHisAspGlnGluGlyGly 48
Db 197 AAAGAACAGAGGGTGGCGAGATGCTCCCTTCACCTGCTTGACCAGAACAGGCGAGGT 256
Qy 49 AlaAlaLeuIleArgAsnAsnMetGlnHisIleMetGlyProValThrAlaIleLysLeu 68
Db 257 GCCACCTCTCTCAGAAATATCATCTAGCTGTAAAGAGTCTGTGACGGGACTGAAGTA 316
Qy 69 LeuGlyGluGluAsnLysGluAsnThrProArgAsnValLeuAsnIleIleProAlaSer 88
Db 317 CAGAGCGACAGAACAAAGAGAGAAACCTCAGAGTGTCTAAGCGTAATTCACACAGAT 376
Qy 89 MetAsnTyraLysAlaHisSerLysLysLysLysProGlnArgAspSerGlnAla 108
Db 377 GTCCACAATACTAACGACTACTCAGAGATACAGAGAACCAACAGAGGGATCTACTACT 436
Qy 109 GlnLysSerProValLysSerLysSerThrHisArgIleGlnHisAsnIleAspTyLeu 128
Db 437 CAGACAGCCCGAGGACAAAGCAACACACCCCTCGGGCCCGAGAGCAGCAGCTACCTA 496
Qy 129 LysHisLeuSerLysValLysLysLysLysLysProSerAspPheGluGlySerGlyThrAsp 148
Db 497 ACACATCTCCCCAAATCAGAAAGATTCTCAGTGACTTCGAGGACAGTGTCTCCCGAGC 556
Qy 149 LeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGlnProPheLys 168
Db 557 CTCTAGTAGGGGGGATTAATGATGTCCTCTTTTCTAGTGGAGATGAGACACATTTATG 616
Qy 169 AspIleProGlyLysGlyGluAlaThrGlyProAspLeuGlu-----GlyLysAsp 185
Db 617 CACACTCCCGACAGAGAGGTGCTGTGGATCTGTGATCTGAAAGCTCAGTGTGTCACCCCT 676
Qy 186 IleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAspThrLysLys 205
Db 677 GTG-----TCAGGCTCCAGCAATGTCGAGATTGTTGACCCACACAGCAATGGA 724
Qy 206 ProGlyTyraAsnGluIleProGluArgGluGluAsnGlyLysAsnThrIleGlyThrArg 225
Db 725 CTGGGCTTAATGAGATCCCGAGGAGAGAGGTCACATAGGCGGTGCTATGCAACCCAGA 784
Qy 226 AspGluThrAlaLysGluAlaAspAlaValSerLeuValGluGlySerAsnAsp 245
Db 785 GGAATAACTGCGAGGGGGCAGGTTCGGCGATGTGAGCCTTGTGGAGGCGAGCAATGAA 844

QY 246 IleMetGlySerThrAsnPhelysGluLeuProGlyArgGluGlyAsnArgValaspala 265
 DB 845 ATCACGGCAGTACCAAAATTTAGGAGCTCCCTGGAAAAGAGGAAACAGAGTCGATGCC 904
 QY 266 GlySerGlnAsnAlaHisGlnGlyValGluPheHisThrProAlaProSerLys 285
 DB 905 AGCAGCCAAATGCTCATCAGGAAAGTAGATTTCTACTCCCAAGCGCCCTCAAAA 964
 QY 286 GluLysArgLysGluSerSerAspAlaAaGluSerThrAsnTyrAsnGluLeuPro 305
 DB 965 GAGAGGTAAAGGGGGCAGCAGGAGCACACAGGGGAAAGCGGTACAATGAAATCCCC 1024
 QY 306 LysAsnGlyLysSerThrArgLysGlyValAspHisSerAsnArgGlnAlaThr 325
 DB 1025 AAGAGCAGCAGGCGCGCTAGCAAGATGCGGAAGATCTAAAGGGAGACCAAGTAACC 1084
 QY 326 LeuAsnGluLysGlnArgPheProSerLysGlyLysSerGlnGlyLeuProfileProSer 345
 DB 1085 TTGACTGAAAGCCAAAGGTTCCAGGCAAAAGGCAGAGCCAGTCT-----TCT 1132
 QY 346 ArgGluLeuAspAsnGluLysAsnGluMetAspSerPheAsnGlyProSerHisGlu 365
 DB 1133 CACAGTCTTGATGAGGTAAAGTGAAGAGACTCTTCTAATAGTCTCAGTAGAGAG 1192
 QY 366 AsnIle---IleThrHisGlyArgLysTyrHisTyrValProHisArgGlnAsnSer 384
 DB 1193 GGGATTGCAATACACACAGGAGCAACAGCCAC-----CCT 1228
 QY 385 ThrArgAsnLysGlyMetProGlnGlyLysGlySerTyr---GlyArgGlnProHisSer 403
 DB 1229 ACACGAATAGGGGATGTACAGCGGAGAGGCTCTCTGGCTCGAGAGACCCCATCCC 1288
 QY 404 AsnArgArgPheSerSerArgArgAspAspSerSerGluSerSerAspSerGlySer 423
 DB 1289 CACCGGCGGTAGACACCCGCCAAGA---GACAGTAGTGATCATCATCCAGTGGAGT 1345
 QY 424 SerSerGluSerAspGlyAsp 430
 DB 1346 TCTAGCAGACGAGTGGTGAC 1366

RESULT 11

; Sequence 39715, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ. ID NOS: 47374
 ; SEQ. ID NO 39715
 ; LENGTH: 1189
 ; TYPE: DNA
 ; ORGANISM: Xanthomonas campestris
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)...(1189)
 ; OTHER INFORMATION: unsure at all n locations
 ; US-10-369-493-39715

Alignment Scores:

Pred. No.: 3,43e-05 Length: 1189
 Score: 149.50 Matches: 91
 Percent Similarity: 36.16% Conservative: 41
 Best Local Similarity: 24.93% Mismatches: 143

Query Match: 6.56% Indels: 90
 DB: 15 Gaps: 20
 US-09-700-696C-2 (1-430) x US-10-369-493-39715 (1-1189)
 QY 70 GlyGluGluAsnLysGluLeuThrProArgAsnValLeuAsnIleIleProAlaSerMet 89
 DB 252 GGGAAATAACGGAAGAACCACC----- 275
 QY 90 AsnTyrAlaLysAlaHisSerLysAspLysLysProGlnArgAspSerGlnAlaGln 109
 DB 276 -----GCGAAGAACAAGACCGCGGAGCGCGGAGCGCGCAAGGAAACAAACACAAA 329
 QY 110 LysSerProValLysSerThrHisArgGlnHisAsnIleAspTyrLeuLys 129
 DB 330 ACCCGGACACAAAAGCCCCGAGCCCGCCCGGAGAACCGAAGAACCGGAAACCGGAAA 389
 QY 130 HisLeu-----SerLysValLysLysIleProSerAspPheGluGlySer 144
 DB 390 AAAAAAGGGGGAACGGGAAACAAGAGTGAACAAACAAACCGCAGAAAAACACAGA 449
 QY 145 GlyTyrThrAspLeuGln-GluArg-----GlyAspAsnAspIleSerProPh 160
 DB 450 AGACACACAAAGAGAGAGACGACGACAAAGCAAGCGGCGGAGAGAGAGCGCCCGGAA 509
 QY 160 eSerGlyAspGlyGln-----ProPheLysAsp---IleProGlyLysGlyGluAl 176
 DB 510 GGGAGGGGAAGAAGACACACAGCCACCCCGGAAGGAGGAAACCGCGGGGCACACCGAAC 569
 QY 176 aThrGlyProAspLeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAl 196
 DB 570 AACC-----CAAGAGGGAAGGAATGAAATACC-----ACAGGACCAAGACCGGC 614
 QY 196 aGluSerThrHisLeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluG 216
 DB 615 GACGGGCAACACCGACCCAGGAAACCGGAGGA-----GACCAACCCACAAACAAA 668
 QY 216 uAsnGlyGlyAsn-----ThrIleGlyThrArgAspG 227
 DB 669 A-----GGGAACGAGACAAAAGCGCGCGCGATAGACAGAAACGAAACCGACCA 722
 QY 227 uThrAlaLysGluAlaAspAlaValAspValSerLeuValGluGlySerAsnAspIleMe 247
 DB 723 AACAGGAAGCGAAGGAGCGCA-----CGAAACAAACACCGACCCCT 764
 QY 247 tGlySerThrAsnPhelysGluLeuProGlyArgGluGlyAsnArgValaspalaglyse 267
 DB 765 CGGACACACAGAGCGCGCAGAA---AAGCAAGAAGAGGCGCAACCGACGAAACCGAGAG 819
 QY 267 rGlnAsnAlaHisGlnGlyLysValGluPheHisTyrPro----- 280
 DB 820 -----GGGCACCCCAAGCAACACGACGACAGCCCGGACGAGAGGAGACAGA 872
 QY 281 -ProAlaProSerLysGlyLysArgLysGluGlySerSerAspAlaAlaGluSerThrAs 300
 DB 873 GAAACCCGACGCGCGGAGAGGACAGAGAAACAAACAAAGAACCAACGAAACCGAGAG 932
 QY 300 nTyrAsnGluLeu-----ProLysAsn-----GlyLysGlySerThrArgly 314
 DB 933 AGAGAACGAGATACCGGAGCAGCAGAGAAACAAACCCCGAGGAGAGGAGCGGAGCGC 992
 QY 314 sGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProse 334
 DB 993 ACGGGAAGAACACACACAGAAAGGAGCCAAACCGCGCAAC-----CCGAA 1037
 QY 334 rLysGlyLysSerGlnGlyLeuProLleProSerArgGlyLeuAspAsnGluLeuLysAs 354
 DB 1038 CCGAGGGAAGCGACCC-----GACAAAGGGGCGCAAGG 1070
 QY 354 nGluMetAspSerPheAsnGlyProSerHisGluAsnIleIleThrHisGlyArgLysTyr 374
 DB 1071 ACAGACGGGAAACACACACAGACACACAGG-----AGGGGACGACAGAA 1118

QY 374 rHisTyrValProHisArgGlnAsnSerThrArgAsnLysGlyMetProGlnGlyLy 394
 Db 1119 CCACACCAAGG-----CAGCAGACCGAGCGGAGCAACACACACCGGAGGACG 1169
 QY 394 sGlySerTrpGly 398
 Db 1170 AGGAGGACCAAGGC 1182

RESULT 12

US-10-363-798-1
 ; Sequence 1, Application US/10363798
 ; Publication No. US20030180280A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kong, Xiangyin
 ; APPLICANT: Xiao, Shuangxi
 ; APPLICANT: Zhao, Guoping
 ; APPLICANT: Yu, Chuan
 ; APPLICANT: Hu, Landian
 ; TITLE OF INVENTION: METHOD OF DIAGNOSING AND TREATING DENTINOGENESIS IMPERFECTA
 ; TITLE OF INVENTION: TYPE II USING DENTIN SIALOPHOSPHOPROTEIN GENE AND CODED
 ; FILE OF INVENTION: PRODUCT THEREOF
 ; FILE REFERENCE: 9548.78USWO
 ; CURRENT APPLICATION NUMBER: US/10/363,798
 ; PRIOR FILING DATE: 2003-03-05
 ; PRIOR FILING DATE: 2000-09-05
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 8201
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-363-798-1

Alignment Scores:

Pred. No.: 0.000536 Length: 8201
 Score: 148.50 Matches: 92
 Percent Similarity: 38.43% Conservative: 84
 Best Local Similarity: 20.09% Mismatches: 218
 Query Match: 6.52% Indels: 64
 DB: 14 Gaps: 14

US-09-700-696c-2 (1-430) x US-10-363-798-1 (1-8201)

QY 4 GluTyrSerIleSerAsnLysGluAsnThrHisAsnGlyLeu-ArgMetSerIleTyrPr 23
 Db 5214 AAATATTCATAGTTAATCATCTTTCTCCATCCTTCCATAGGGAATAGAAATCAAGG 5273
 QY 23 oLysSerThrGlyAsnLysGlyPhe-----GluAspGlyAspAspAlaIleSerLysLe 41
 Db 5274 TCCACGACGTGGCAACAGAAATATTACCAAGAGTTGGAAAGGCAACGAAAGGTAAA-- 5331
 QY 41 uHisAspGlnGluTyrGlyAlaAlaLeuIleArgAsnAsnMetGlnHisIleMetGl 61
 Db 5332 -GAGGATAAGGACAAACATGGATGATCTTTGGCAAGCAATGTCAAG---ACACAAGG 5387
 QY 61 yProValThrAlaIleLysLeuLeuGlyGluGluAsnLysGluAsnThrProArgAsnVa 81
 Db 5388 AGAGGTGTTCACATAGAGACCTGCGCCAAATCAAG-----CCAGGAATATA 5438
 QY 81 lLeu-----AsnIl 84
 Db 5439 AGTTGGACACAGCAATACAGGTAGTGACGCAATAGTGTGATGATGACAGTTATGTTT 5498
 QY 84 eIleProAlaSerMetAsnTyrAlaLysAlaHisSerLysAspLysLysProGlnAr 104
 Db 5499 TGATGATAGTCCATCCAGGAGATGATCCCATAGCAGTGTGATGATCTAATGGCAATGA 5558
 QY 104 gAspSerGlnAlaGlnLysSerProValLysSerThrHisArgIleGlnHis 124
 Db 5559 TGATGCTAATTCAGAA---AGTGACAATAACAGCAGTACCGGAGGAGATGCTTCTTATAA 5615
 QY 124 nIleAspTyrLeuLysHisLeuSerLysValLysLysIleProSerAspPheGluGlySe 144

Db 5616 CTCTGATGAA-----TCAAAAGATAATGCAATGCGAGTGCCTCAAAAGGAGC 5663
 QY 144 rGlyTyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGl 164
 Db 5664 AGAAGATGATGACAGTGTAGCAGCATCAGCACTAATAATAGTACAGTAATGGCAATGG 5723
 QY 164 yGlnProPheLysAsp-----lLeProGlyLysGlyGluAlaThrGlyPr 179
 Db 5724 TAACATGGGAATGATGACAATGACAATCAGACAGTGGCAAAAGGTAAATCAGATAGCAG 5783
 QY 179 oAspLeuGluGlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerTh 199
 Db 5784 TGACAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGA 5843
 QY 199 rHisLeuAspThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGl 219
 Db 5844 CACGAGTGTAGCAACAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGA 5903
 QY 219 yAsnThrIleGlyThrArgAspGluThrAlaLysGluAlaAspAlaValAspValSerLe 239
 Db 5904 CAGTGTAGTGTAGTGTAGTGTAT---AGCAGCAATAGCAGTGTAGTGTAGTGTAGTGTGA 5960
 QY 239 uValGluGlySerAsnAspIleMetGlySerThrAsnPheLysGluLeuProGlyArg-- 258
 Db 5961 TAGCAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGA 6020
 QY 259 -----GluGlyAsnArgValAspAlaGlySerGlnAsnAlaHisGlnGlyLysValGl 276
 Db 6021 AGAGAGCGACAGCAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGA 6080
 QY 276 uPheHisTyrProProAlaProSerLysGluLysArgLysGluGlySerSerAspAlaAl 296
 Db 6081 CAGTGTGTGCAACAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 6140
 QY 296 aGluSerThrAsnTyrAsnGluIleProLysAsnGlyLysGlySerThrArgLysGlyVa 316
 Db 6141 TGACAGCAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 6195
 QY 316 lAspHisSerAsnArgAsnGlnAlaThrLeuAsnGluLysGlnArgPheProSerLysGl 336
 Db 6196 -GACAGCAACAGCAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 6254
 QY 336 yLysSerGlnGlyLeuProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMe 356
 Db 6255 CAGTGTAGT-----AGTGACAGCAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGA 6299
 QY 356 tAspSerPheAsnGlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHisTy 376
 Db 6300 TGACAGCAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 6330
 QY 376 rValProHisArgGlnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySe 396
 Db 6331 -----GACAGCAGCAACAGCAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 6380
 QY 396 rTrpGlyArgGlnProHisSerAsnArgPheSerSerArgArgAsp-----413
 Db 6381 CAGCAACAGCAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTGA 6440
 QY 414 -----AspSerSerClusSerSerAspSerGlySerSerSerGluSerAsp 428
 Db 6441 TAGCAGTGTAGCAGCAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGA 6492

RESULT 13

US-10-108-260A-1338
 ; Sequence 1338, Application US/10108260A
 ; Publication No. US20040005560A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: NO. US20040005560A1e1 full length cDNA
 ; FILE REFERENCE: HI-A0106
 ; CURRENT APPLICATION NUMBER: US/10/108,260A
 ; CURRENT FILING DATE: 2002-03-27

; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1338
; LENGTH: 3045
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-260A-1338

Alignment Scores:
Pred. No.: 0.000165 Length: 3045
Score: 148.00 Matches: 106
Percent Similarity: 34.76% Conservative: 85
Best Local Similarity: 21.54% Mismatches: 209
Query Match: 6.49% Indels: 112
DB: 15 Gaps: 24

US-09-700-696C-2 (1-430) x US-10-108-260A-1338 (1-3045)

```
QY 1 ValAsnLysGluTyrSerIleSerAsnLys-----GluAsnThrHisAsnGly 16
Db 119 GTAACGCGAAGCATCACATTAAGGAAAGAGGAGGGAGTTCCAGGAATCCAGAGGGGC 178
QY 17 Leu-----ArgMetSerIleTyrPro 23
Db 179 CTGGTACAGATGAGACAGATAGAGGATGAATCAAGAGGCGATGACTGTGCACAGT 238
QY 24 LysSerThrGlyAsnLys-----GlyPheGluAspGlyAspAlaIle 38
Db 239 TCTGTTTCCACAGCAATAACCTCAACTCTATGCCAGCTGCTGAAAGGGGTAAAGACACATTA 298
QY 39 SerLysLeuHisAspGlnGluGlu-----TyrGlyAlaAlaLeu-----IleArgAsn 54
Db 299 AATATCAGCTATATGATACAGAAATGACCTAAAGAGGAGCAGCTATTCTATCTCAAAA 358
QY 55 AsnMetGlnHisIleMetGlyProValThrAlaIleLysLeuLeuGlyGluGluAsnLys 74
Db 359 GGAATGCTCCACGAAGAAAGCCCTGGAGAGCAGCATTTTGAAGGTGGCTCAGAGATGAA 418
QY 75 -----GluAsnThrProArgAsnValLeuAsn-----IleIleProAlaSerMet 89
Db 419 TCTGCACAGAAAGCTGCAGGAGATCAATGATGACAGAAAGATTCAACAGGATCCCTG 478
QY 90 AsnTyrAlaLysAlaHisSerLysLysLysLysProGlnArgAspSerGlnAlaGln 109
Db 479 GGTAGTGCACCACTCATGGAGATGACCCCTTAAGCATCCAGACAGCATGTGGAGGGA 538
QY 110 LysSerProValLysSerLysSerThrHis-----ArgIleGlnHisAsnIleAspTyr 127
Db 539 GACCTTTGGTAAATGGGGCCAACTGCACACGCTTTCAGTGGAGCATCACTGAGGAA 598
QY 128 LeuLysHis-----LeuSerLysValLysLysLysIleProSerAspPheGluGlySerGly 145
Db 599 TTGAAGAGGAGTATAGTTCTTAAACTCAAAACCAACCTAGA--TTCTCTCTCCAGAT 655
QY 146 TyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGln 165
Db 656 GAGATTGATTGGCCAGAGACTCGAAGACGAGGTT--CCCATTTCTGGGAAAGAAATCTT 712
QY 166 ProPhe-----LysAspIleProGlyLysGlyGluAlaThrGlyProAspLeuGlu 182
Db 713 CCCTGGCAACAAGAAAGAGATGTG-----GCTGCCACAGCCAGTAAAGCAATG 760
QY 183 GlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAsp 202
Db 761 AGTGAGAGATPAAG-----CTCTGTGAGGAGAAAGCAAGAGGAGTCTCTGGAT 811
QY 203 ThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIle 222
Db 812 -----GAGAGATTTTTCATCAGAGGCAATGCGAGGCGACAGAGGTA 853
QY 223 GlyThrArgAspGluThr-----AlaLysGlu 231
Db 854 GGACAGACAGACCAACTGACAGCAGAGGAGGACCGCTTTCTTTCTTAAGTAGAAGAG 913
```

```
QY 232 AlaAspAlaValAspValSerLeuValGluGlySerAsnAspIleMetGlySerThrAsn 251
Db 914 GATGATATTCCTCTGAGAGACTACTAGAGATGAAACGCTATAAATGCAAAACGGTCT 973
QY 252 PheLysGluLeuProGlyArgGluGlyAsnArgValAspAlaGlySerGln-----268
Db 974 AAAGAAAAAACCCGGGGAATCAGGCGCAGCTTTGATGTTGATTAATCTGCAAGTCCCTGAC 1033
QY 269 AsnAlaHisGlnGlyLysValGluPheHisTyrProProAlaProSerLysGlyLysArg 288
Db 1034 AGAGCAGTTTATAGGACCATTCAT-----CCAGATCCAGAAATTTGAAGAAAGC 1081
QY 289 LysGluGlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluIleProLysAsnGly 308
Db 1082 AAGCAAGAAACTAGTATGATTTTGGATAGTGAAGAAACAAAGTGAG-----1126
QY 309 LysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGlu 328
Db 1127 -----ACTGCTGCCAAGGGGTCAACACAGGAGGCGGACCAAAATACATGGTGGAA 1180
QY 329 LysGlnArg-----PheProSerLysGlyLysSer 338
Db 1181 AAAGACGCGCTCTGGCAGATAAGAAAGCAGAGACCATTTGACGAAAGTGACTTTTCT 1240
QY 339 GlnGlyLeuProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSer 358
Db 1241 GACAGATAAATTCAGACTCCAGATTAGGTGAGTGTTCAGATTAAGATTCTTGAT 1300
QY 359 Phe-----AsnGlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHisTyr 376
Db 1301 TATCTGAAGACGACCAACCTCTGAGAAACATCTGAAGACCTCAGGGCTT-----1348
QY 377 ValProHisArgGlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySer 396
Db 1349 -----GCAGGGGAGCTGAGGGAGAACTCTCA 1375
QY 397 TrpGlyArgGlnProHisSerAsnArgPheSerSerArgArgArgAspAspSerSer 416
Db 1376 -----AAAGAGGACCATGAGAAC-----ACAGAGAGTACATGGGCACA 1414
QY 417 GluSerSerAspSerGlySerSerSerGluSerAsp 428
Db 1415 GAAAGCCAGGGGTCTGCTGTCGAGAAACCTGAAGAT 1450
```

RESULT 14

```
US-10-210-172-65
; Sequence 65, Application US/10210172
; Publication No. US20040043928A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Miller, Charles
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol
; APPLICANT: Rieger, Daniel
; APPLICANT: Shinkets, Richard
; APPLICANT: Zethusen, Bryan
; APPLICANT: Li, Li
; APPLICANT: Ji, Weizhen
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Casman, Stacie
; APPLICANT: Voss, Edward
; APPLICANT: Boldog, Ferenc
; APPLICANT: Gorman, Linda
; APPLICANT: Leite, Mario
; APPLICANT: Vernet, Corine
; APPLICANT: Anderson, David
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zhong, Mei
; APPLICANT: Gerlach, Valerie
; APPLICANT: Hjalte, Tord
; APPLICANT: Rastelli, Luca
; APPLICANT: Spytek, Kimberly
```

; APPLICANT: Edinger, Shlomit
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Malyankar, Uriel
 ; APPLICANT: MacDougall, John
 ; APPLICANT: Stone, David
 ; APPLICANT: Alsobrook II, John
 ; APPLICANT: Lepley, Denise et al.
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
 ; FILE REFERENCE: 21402-416 A US/10/210,172
 ; CURRENT APPLICATION NUMBER: 2001-08-01
 ; PRIOR FILING DATE: 2001-08-01
 ; PRIOR APPLICATION NUMBER: 60/309,501
 ; PRIOR FILING DATE: 2001-08-02
 ; PRIOR APPLICATION NUMBER: 60/323,994
 ; PRIOR FILING DATE: 2001-09-21
 ; PRIOR APPLICATION NUMBER: 60/373,814
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: 60/310,291
 ; PRIOR FILING DATE: 2001-08-03
 ; PRIOR APPLICATION NUMBER: 60/310,951
 ; PRIOR FILING DATE: 2001-08-08
 ; PRIOR APPLICATION NUMBER: 60/310,544
 ; PRIOR FILING DATE: 2001-08-07
 ; PRIOR APPLICATION NUMBER: 60/311,292
 ; PRIOR FILING DATE: 2001-08-09
 ; PRIOR APPLICATION NUMBER: 60/311,979
 ; PRIOR FILING DATE: 2001-08-13
 ; PRIOR APPLICATION NUMBER: 60/313,201
 ; PRIOR FILING DATE: 2001-08-17
 ; PRIOR APPLICATION NUMBER: 60/312,892
 ; PRIOR FILING DATE: 2001-08-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 327
 ; SOFTWARE: Curaseq! version 0.1
 ; SEQ ID NO 65
 ; LENGTH: 4985
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:

; NAME/KEY: CDS
 ; LOCATION: (13)..(4785)
 US-10-210-172-65

Alignment Scores:
 Pred. No.: 0.000314 Length: 4985
 Score: 148.00 Matches: 106
 Percent Similarity: 34.76% Conservative: 65
 Best Local Similarity: 21.54% Mismatches: 209
 Query Match: 6.49% Indels: 112
 DB: 12 Gaps: 24

US-09-700-696c-2 (1-430) x US-10-210-172-65 (1-4985)

QY 1 ValAsnLysGluTyrSerIleSerAsnLys-----GluAsnThrHisAsnGly 16
 DB 1384 GTAAACCGACACATCACATTAAAGGAAAGGGAGGGAGTTCCAGGATCCAGAGGGGC 1443
 QY 17 Leu-----ArgMetSerIleTyrPro 23
 DB 1444 CTGGTACACATTAAGACAGAAATAGAGGTGAATAATCAAGAGGGCATGCTGACAGCT 1503
 QY 24 LysSerThrGlyAsnLys-----GlyPheGluAspGlyAspAlaIle 38
 DB 1504 TCTGTTCCACAGCAATAACCTCACTCTATGCCAGCTGCTGAAAGGGTAAAGACACATT 1563
 QY 39 SerLysLeuHisAspGlnGlu-----TyrGlyAlaAlaLeu-----IleArgAsn 54
 DB 1564 AATACAGCTTATGATACAGAAATGACCTAAAGAGGAGCAGCTATTCTATCTCAAAA 1623
 QY 55 AsnMetGlnHisIleMetGlyProValThrAlaIleLysLeuGlyGluGluAsnLys 74
 DB 1624 GGAATGCTCCACGACGAAAGCCCTGGAGAGCAGATTTTGAAGGTGGCTCAGAGATGAA 1683

QY 75 -----GluAsnThrProArgAsnValLeuAsn-----IleIleProAlaSerMet 89
 DB 1684 TCTGCACAGAAAGCTGCAGGGAATCAATGAATGACAGAAAGATTCAACAGGATCCCTG 1743
 QY 90 AsnTyrAlaLysAlaHisSerLysAspLysLysProGlnArgAspSerGlnAlaGln 109
 DB 1744 GGTAGTCCACCACTCATGAGGAGATGACCCCTAACGCATCCACAGACAGCTGTGGAGGA 1803
 QY 110 LysSerProValLysSerLysSerThrHis-----ArgIleGlnHisAsnIleAspTyr 127
 DB 1804 GAGCTTTTGGTAAATGGGCCAACTGCACACGCTTTCAGTGGAGCATCAACGTGAGGAA 1863
 QY 128 LeuLysHis-----LeuSerLysValLysLysIleProSerAspPheGluGlySerGly 145
 DB 1864 TTGAACAGAGGAATTAGTTCTTAAACTCAAAACCACTAGA--TTCTCTCTCCAGAT 1920
 QY 146 TyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGln 165
 DB 1921 GAGATTGATTTGCCAGAGAACTGGAGACGAGGTT---CCCATCTGGGAAGAAATCTTT 1977
 QY 166 ProPhe-----LysAspIleProGlyLysGlyGluAlaThrGlyProAspLeuGlu 182
 DB 1978 CCTGGCAACAGAAACAGATGTG-----GCTGCCACGCCAGTAAACCAATG 2025
 QY 183 GlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAsp 202
 DB 2026 AGTGAGAGAGTAAGG-----CTCTCTGAGGAGAGCAAGCAAGAGGAGCTCCTTGAT 2076
 QY 203 ThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIle 222
 DB 2077 -----GAAGAGTTTTTTCATCACAGGCAATGCGGGCACAGAGTA 2118
 QY 223 GlyThrArgAspGluThr-----AlaLysGlu 231
 DB 2119 GGACAGACAGACCAAACTGACAGCAGGAGGACCAGCTTTCCTTTCTAAAGTAGAAGAG 2178
 QY 232 AlaAspAlaValAspValSerLeuValGluGlySerAsnAspIleMetGlySerThrAsn 251
 DB 2179 GATGATTATCCTCTGAGAACTACTAGAGGATGAAACCGCTATTAATGCAAAACGGTCT 2238
 QY 252 PheLysGluLeuProGlyArgGluGlyAsnArgValAspAlaGlySerGln----- 268
 DB 2239 AAGAAAAAAACCTCGGAATCAGGCGAGGAGCTTTGATGTTAATCTGCAAGTCCCTGAC 2298
 QY 269 AsnAlaHisGlnGlyLysValGluPheHisTyrProProAlaProSerLysGlyLysArg 288
 DB 2299 AGACGAGTTTTAGGCGACCATTCAT-----CCAGATCCAGAAATGAAGAAAGC 2346
 QY 289 LysGluGlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluIleProLysAsnGly 308
 DB 2347 AAGCAGAAACTAGTATGATTTTGGATAGCGAAAAAACAAGTCAG----- 2391
 QY 309 LysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGlu 328
 DB 2392 -----ACTGCTGCAAAAGGGTCAACACAGGAGGCGGAGCAACCAATAACAAATGAGTGA 2445
 QY 329 LysGlnArg-----PheProSerLysGlyLysSer 338
 DB 2446 AAGAACGCCCTCTGCAGATAAGAACACAGACAGCCATTGACGAGTACTTTTCT 2505
 QY 339 GlnGlyLeuProLysProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSer 358
 DB 2506 GACAGCATAAAATTCAGATCCAGATTAAGTGAAGTGTTCAGATAAAGATTTCTGAT 2565
 QY 359 Phe-----AsnGlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHisTyr 376
 DB 2566 TATCTGAAGAACGACCAACCTCTGAGGAACATCTGAGACCTCAGGGCTT----- 2613
 QY 377 ValProHisArgGlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySer 396
 DB 2614 -----CGAGGGAGGCTGAGGAGAACTCTCA 2640
 QY 397 TrpGlyArgGlnProHisSerAsnArgArgPheSerSerArgArgAspAspSerSer 416

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Db 2641 -----AAAGAGGACCATGAGAC-----ACAGAGAGTACATGGGCACA 2679
Qy 417 GluSerSerAspSerGlySerSerGluSerAsp 428
Db 2680 GAAAGCCAGGGGTCTGCTGCTGCAGAAACCTGAAGAT 2715

RESULT 15
US-09-785-770A-15
; Sequence 15, Application US/09785770A
; Patent No. US20020103360A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; INVENTOR: Barnes, Thomas M.
; TITLE OF INVENTION: A NOVEL PROTEIN RELATED TO MELANOMA-INHIBITING PROTEIN
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 07334-328001
; CURRENT APPLICATION NUMBER: US/09/785,770A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: US 09/387,462
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: US 09/145,056
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in Ver. 4.0
; SEQ ID NO 15
; LENGTH: 5721
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(5721)
US-09-785-770A-15

Alignment Scores:
Pred. No.: 0.000375 Length: 5721
Score: 148.00 Matches: 106
Percent Similarity: 34.76% Conservative: 65
Best Local Similarity: 21.54% Mismatches: 209
Query Match: 6.49% Indels: 112
DB: 9 Gaps: 24

US-09-700-696C-2 (1-430) x US-09-785-770A-15 (1-5721)
Qy 1 ValAsnLysGluTyrSerIleSerAsnLys-----GluAsnThrHisAsnGly 16
Db 1372 GTAAACCAGACATCATTAAGGAAGGGGGAGTTCCAGGAATCCAGAGGGGC 1431
Qy 17 Leu-----ArgMetSerIleTyrPro 23
Db 1432 CTGGTACAGATGAGACAGAAATTAGAGGATGAAATCAAGAGGCATGACTGTGCACAT 1491
Qy 24 LysSerThrGlyAsnLys-----GlyPheGluAspGlyAspAlaIle 38
Db 1492 TCTGTTTACAGCAATAACCTCAACTCTATGCCAGCTGCTGAAAGGTAAGACACATTA 1551
Qy 39 SerLysLeuHisAspGlnGlu-----TyrGlyAlaAlaLeu-----IleArgAsn 54
Db 1552 AAATCAGCTTATGATGATACAGAAATGACCTAAAGAGGAGCAGCTATTATATCTCAAAA 1611
Qy 55 AsnMetGlnHisIleMetGlyProValThrAlaIleLysLeuGluGluAsnLys 74
Db 1612 GGAATGCTCCAGNAGAAAGCCCTGGAGACAGATTTTGAAGGTGGCTCAGAGAGTGAA 1671
Qy 75 -----GluAsnThrProArgAsnValLeuAsn-----IleIleProAlaSerMet 89
Db 1672 TCTGCACAGAAAGCTGCAGGGAATCAATGAATGACAGAAAGATTCAACAGGAATCCCTG 1731
Qy 90 AsnTyrAlaLysAlaHisSerLysAspLysLysLysProGlnArgAspSerGlnAlaGln 109
Db 1732 GGTAGTCACACCTCATGAGGAGATGACCCCTAAACGATCCAGACAGACATGTGGAGGGA 1791
Qy 110 LysSerProValLysSerLysSerThrHis-----ArgIleGlnHisAsnIleAspTyr 127

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Search completed: March 29, 2004, 04:28:42

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Db 1792 GACGCTTTGGTAAATGGGGCCAAACTGCACACGCTTTTCAGTGGAGCATCAACGTGAGAA 1851
Qy 128 LeuLysHis-----LeuSerLysValLysLysLysLysLysLysLysLysLysLysLys 145
Db 1852 TTGAAGAGAGGAATAGTTCTTAAACCTCAAAACCAACCTAGA---TTCTCTCTCCAGAT 1908
Qy 146 TyrThrAspLeuGlnGluArgGlyAspAsnAspIleSerProPheSerGlyAspGlyGln 165
Db 1909 GAGATTGATTTGCCAGAGAACTGGAAGACGAGGTT---CCCATTTCTGGGAAGAAATCTT 1965
Qy 166 ProPhe-----LysAspIleProGlyLysGlyGluAlaThrGlyProAspLeuGlu 182
Db 1966 CCCTGGCAACAGAAAGAGATGTG-----GCTCCACAGCCAGCAATAGCAAAATG 2013
Qy 183 GlyLysAspIleGlnThrGlyPheAlaGlyProSerGluAlaGluSerThrHisLeuAsp 202
Db 2014 AGTGAGAAGATAAGG-----CTCTCTGAGGAGAGCAAGCAAGAGGAGCTCTTGAT 2064
Qy 203 ThrLysLysProGlyTyrAsnGluIleProGluArgGluGluAsnGlyGlyAsnThrIle 222
Db 2065 -----GAAGAGTTTTTTTCATCACAAGGCAATGCGAGGCACAGAGGTA 2106
Qy 223 GlyThrArgAspGluThr-----AlaLysGlu 231
Db 2107 GGACAGACAGACCAACTGCACAGCAGAGGAGCAGCTTCTCTTTCTAAAGTAGAAGAG 2166
Qy 232 AlaAspAlaValAspValSerLeuValGluGlySerAsnAspIleMetGlySerThrAsn 251
Db 2167 GATGATTATCCCTCTGAAGAACTACTAGAGGATGAAACACCTATAAATGCAAAACGGTCT 2226
Qy 252 PheLysGluLeuProGlyArgGluGlyAsnArgValAspAlaGlySerGln----- 268
Db 2227 AAAGAAAAAACCCCGGGGAATCAGGCGAGCAGCTTGATGTTAATCTGCAAGTCCCTGAC 2286
Qy 269 AsnAlaHisGlnGlyLysValGluPheHisTy-ProProAlaProSerLysGluLysArg 288
Db 2287 AGAGCAGTTTTAGGAGCATTTCAT-----CCAGATCCAGAAATTTGAAGAAAGC 2334
Qy 289 LysGluGlySerSerAspAlaAlaGluSerThrAsnTyrAsnGluIleProLysAsnGly 308
Db 2335 AAGCAAGAACTAGTATGATTTGGATGTAAGAAAAACAAGTGAG----- 2379
Qy 309 LysGlySerThrArgLysGlyValAspHisSerAsnArgAsnGlnAlaThrLeuAsnGlu 328
Db 2380 -----ACTGCTGCAAGGGGTCAACACAGAGGAGGAGCAACCAATACAAATGCTGGA 2433
Qy 329 LysGlnArg-----PheProSerLysGlyLysSer 338
Db 2434 AARGAGCCCTCTGGCAGATAGAAAGCAGACAGACCATTTGACCAAGTACTTTTCT 2493
Qy 339 GlnGlyLeuProIleProSerArgGlyLeuAspAsnGluIleLysAsnGluMetAspSer 358
Db 2494 CACAGCATAAATTTAGATCCAGATTTAGTGAAGTTCAGATTAAGATTTCTGAT 2553
Qy 359 Phe-----AsnGlyProSerHisGluAsnIleIleThrHisGlyArgLysTyrHisTyr 376
Db 2554 TATCTGAAGACAGACAACTCTGAGGAACATCTGAAGACCTCAGGGCTT----- 2601
Qy 377 ValProHisArgGlnAsnAsnSerThrArgAsnLysGlyMetProGlnGlyLysGlySer 396
Db 2602 -----GCAGGGGAGCCCTGAGGAGAACTCTCA 2628
Qy 397 TrpGlyArgGlnProHisSerAsnArgPheSerSerArgArgAspAspSerSer 416
Db 2629 -----AAAGAGGAGCATTGAGAAC-----ACAGAAAGATCATGGGCACA 2667
Qy 417 GluSerSerAspSerGlySerSerSerGluSerAsp 428
Db 2668 GAAGCCAGGGGTCTGCTGCTGCAGAACCTCAAGAT 2703

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Job time : 530 secs